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*April 19, 2005*

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**APPLICATION NUMBER: 60/549,865**

**FILING DATE: *March 03, 2004***

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17169 U.S. PTO  
030304

PTO/SB/16 (01-04)

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# PROVISIONAL APPLICATION FOR PATENT COVER SHEET

This is a request for filing a PROVISIONAL APPLICATION FOR PATENT under 37 CFR 1.53(c).

Express Mail Label No. EU 813933419 US

INVENTOR(S)		
Given Name (first and middle [if any])	Family Name or Surname	Residence (City and either State or Foreign Country)
Chaker	Adra	Boston, MA

Additional inventors are being named on the \_\_\_\_\_ separately numbered sheets attached hereto

## TITLE OF THE INVENTION (500 characters max)

IDENTIFICATION OF GRANULOCYTE SUBTYPE-SELECTIVE RECEPTORS AND ION CHANNELS BY USING A HIGH-DENSITY OLIGONUCLEOTIDE PROBE ARRAY

Direct all correspondence to: CORRESPONDENCE ADDRESS

☐ Customer Number:

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## ENCLOSED APPLICATION PARTS (check all that apply)

<input checked="" type="checkbox"/> Specification Number of Pages <u>18</u>	<input type="checkbox"/> CD(s), Number _____
<input checked="" type="checkbox"/> Drawing(s) Number of Sheets <u>35</u>	<input checked="" type="checkbox"/> Other (specify) <u>Attachment 1370</u>
<input type="checkbox"/> Application Data Sheet. See 37 CFR 1.76	

## METHOD OF PAYMENT OF FILING FEES FOR THIS PROVISIONAL APPLICATION FOR PATENT

<input checked="" type="checkbox"/> Applicant claims small entity status. See 37 CFR 1.27.	FILING FEE Amount (\$)  80.00
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The invention was made by an agency of the United States Government or under a contract with an agency of the United States Government.

☐ No.

☒ Yes, the name of the U.S. Government agency and the Government contract number are: NIH Grant AI 43663 from the National Institute of Allergy and Infectious Diseases and by Grant RSG-01-241-01-LIB from the American Cancer Society (to C.A.).

[Page 1 of 1]

Respectfully submitted,  
SIGNATURE [Signature]  
TYPED or PRINTED NAME David S. Resnick  
TELEPHONE (617) 345-6057

Date March 3, 2004  
REGISTRATION NO. 34,235  
(If appropriate)  
Docket Number: 732892-055040-P

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 19487 U.S. PTO  
 60/549863  
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**FEE TRANSMITTAL  
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Effective 10/01/2003. Patent fees are subject to annual revision.

☒ Applicant claims small entity status. See 37 CFR 1.27

TOTAL AMOUNT OF PAYMENT (\$ 80.00

**Complete if Known**

Application Number	To be assigned
Filing Date	Herewith
First Named Inventor	C. Adra
Examiner Name	
Art Unit	
Attorney Docket No.	732892-055040-P

**METHOD OF PAYMENT (check all that apply)**☒ Check ☐ Credit card ☐ Money Order ☐ Other ☐ None☒ Deposit Account:Deposit  
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Large Entity		Small Entity		Fee Description	Fee Paid
Fee Code	Fee (\$)	Fee Code	Fee (\$)		
1001	770	2001	385	Utility filing fee	
1002	340	2002	170	Design filing fee	
1003	530	2003	265	Plant filing fee	
1004	770	2004	385	Reissue filing fee	
1005	160	2005	80	Provisional filing fee	80.00
SUBTOTAL (1) (\$)					80.00

**2. EXTRA CLAIM FEES FOR UTILITY AND REISSUE**

Total Claims		Extra Claims		Fee from below		Fee Paid	
Independent Claims		-20** =		X			
Multiple Dependent		-3** =		X			

Large Entity		Small Entity		Fee Description
Fee Code	Fee (\$)	Fee Code	Fee (\$)	
1202	18	2202	9	Claims in excess of 20
1201	86	2201	43	Independent claims in excess of 3
1203	290	2203	145	Multiple dependent claim, if not paid
1204	86	2204	43	** Reissue independent claims over original patent
1205	18	2205	9	** Reissue claims in excess of 20 and over original patent

SUBTOTAL (2) (\$)

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**FEE CALCULATION (continued)****3. ADDITIONAL FEES**

Large Entity Small Entity

Fee Code	Fee (\$)	Fee Code	Fee (\$)	Fee Description	Fee Paid
1051	130	2051	65	Surcharge - late filing fee or oath	
1052	50	2052	25	Surcharge - late provisional filing fee or cover sheet	
1053	130	1053	130	Non-English specification	
1812	2,520	1812	2,520	For filing a request for ex parte reexamination	
1804	920*	1804	920*	Requesting publication of SIR prior to Examiner action	
1805	1,840*	1805	1,840*	Requesting publication of SIR after Examiner action	
1251	110	2251	55	Extension for reply within first month	
1252	420	2252	210	Extension for reply within second month	
1253	950	2253	475	Extension for reply within third month	
1254	1,480	2254	740	Extension for reply within fourth month	
1255	2,010	2255	1,005	Extension for reply within fifth month	
1401	330	2401	165	Notice of Appeal	
1402	330	2402	165	Filing brief in support of an appeal	
1403	290	2403	145	Request for oral hearing	
1451	1,510	1451	1,510	Petition to institute a public use proceeding	
1452	110	2452	55	Petition to revive - unavoidable	
1453	1,330	2453	665	Petition to revive - unintentional	
1501	1,330	2501	665	Utility issue fee (or reissue)	
1502	480	2502	240	Design issue fee	
1503	640	2503	320	Plant issue fee	
1460	130	1460	130	Petitions to the Commissioner	
1807	50	1807	50	Processing fee under 37 CFR 1.17(q)	
1806	180	1806	180	Submission of Information Disclosure Stmt	
8021	40	8021	40	Recording each patent assignment per property (times number of properties)	
1809	770	2809	385	Filing a submission after final rejection (37 CFR 1.129(a))	
1810	770	2810	385	For each additional invention to be examined (37 CFR 1.129(b))	
1801	770	2801	385	Request for Continued Examination (RCE)	
1802	900	1802	900	Request for expedited examination of a design application	

Other fee (specify)

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**SUBMITTED BY**

(Complete if applicable)

Name (Print/Type)	David S. Resnick	Registration No. (Attorney/Agent)	34,235	Telephone	(617) 345-6057
Signature		Date	3/3/04		

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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of: Chaker Adra  
Application No.: To be assigned                      Group No.: To be assigned  
Filed: Herewith                                      Examiner: To be assigned  
For: IDENTIFICATION OF GRANULOCYTE SUBTYPE-SELECTIVE  
RECEPTORS AND ION CHANNELS BY USING A HIGH-DENSITY  
OLIGONUCLEOTIDE PROBE ARRAY

MAIL STOP PROVISIONAL APPLICATION

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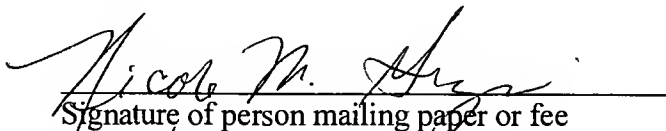
Date of Deposit: March 3, 2004

I hereby state that the following *attached* papers and fees:

1. Provisional Application for Patent Cover Sheet (1 pp.);
2. Provisional Patent Application (1423 pp.): Specification – 18 pp.; Drawings – 35 sheets; Attachment – 1370 pp.;
3. Fee Transmittal (1 pg.);
4. Check in the Amount of \$ 80.00;
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Nicole M. Gignac

  
Signature of person mailing paper or fee

## IDENTIFICATION OF GRANULOCYTE SUBTYPE-SELECTIVE RECEPTORS AND ION CHANNELS BY USING A HIGH-DENSITY OLIGONUCLEOTIDE PROBE ARRAY

**[0001]** This invention was made in part with U.S. Government support under NIH Grant AI 43663 from the National Institute of Allergy and Infectious Diseases and by Grant RSG-01-241-01-LIB from the American Cancer Society (to C.A.). The U.S. Government has certain rights in this application.

### FIELD OF THE INVENTION

**[0002]** The present invention relates to the identification of granulocyte subtype-selective receptors and ion channels that can be use as targets for drug discovery.

### BACKGROUND OF THE INVENTION

**[0003]** Three types of human blood granulocytes, eosinophils, basophils and neutrophils, play roles in protecting against microbial infection by releasing cell type-specific mediators and proteases. Specifically, eosinophils and basophils evoke allergic reactions as well as damage nematodes.<sup>1,2</sup> As well as killing bacteria, neutrophils sometimes induce systemic vasculitis or multiple organ damage under certain conditions.<sup>3,4</sup> Thus, targeting granulocyte type-selective functions is considered an important strategy for drug discovery.

**[0004]** Activation of blood granulocytes and tissue mast cells is generally characterized by an influx of extracellular calcium ( $\text{Ca}^{2+}$ ), which is essential for subsequent release of granule-derived mediators, newly generated lipid mediators and cytokines.<sup>5</sup> The mechanism by which granulocyte mediator secretion is sustained is therefore likely to include modulation of various types of ion channels. Flow of ions including  $\text{K}^{+}$  and  $\text{Cl}^{-}$  may play an important role during granulocyte responses because they regulate cell membrane potential and thus influence  $\text{Ca}^{2+}$  influx.<sup>6</sup> Treatment of mast cells and basophils with pertussis toxin inactivates the  $\text{Gi}$ -type of G-proteins and abolishes degranulation induced by non-immunological ligands such as thrombin and N-formylpeptide; however, it fails to inhibit the influx of  $\text{Ca}^{2+}$ .<sup>7</sup> Thus,  $\text{Ca}^{2+}$ -independent

stimulation of Gi is also involved in granulocyte degranulation. The thrombin (protease) activated receptors and formylpeptide receptors are classified as G protein-coupled receptors (GPR), having an extracellular N-terminal segment, a seven transmembrane region, which forms the transmembrane core; three exoloops, three cytoloops, and a C-terminal segment.<sup>8</sup> Thus, ion channels and GPR both play essential roles in degranulation as well as other cellular function important for granulocytes. As a result, both ion channels and GPR are targets of drug development.<sup>9</sup>

**[0005]** As the human genome project nears completion, the identification of potential drug targets using gene expression profiles from specific cell types is becoming practical and important for drug discovery.<sup>10,11</sup> The sequencing of the human genome is offering an unprecedented opportunity for the pharmaceutical development of drugs. Receptor genes and ion channel genes are found only in 5% and 1.3% of all genes present in the human genome,<sup>10</sup> respectively. However, receptors and ion channels are respectively found in 45% and 5% of the molecular targets of all known drugs.<sup>9,12,13</sup> Thus, receptors including GPR and ion channels are now considered as the most important drug targets.

**[0006]** Until recently, it has been impractical to analyze genome-wide expression of leukocytes. Newly developed technology, the microarray or high density oligonucleotide probe array (GeneChip) is one of the latest breakthroughs in experimental molecular biology, which allows approximately 39,000 transcripts derived from a cells transcriptome to be simultaneously monitored. Using this technology, we previously reported the transcriptome profiling of various types of mast cells and eosinophils.<sup>14-16</sup> However, there is still a need in the art to identify drug targets that are selectively, or preferentially, expressed in specific cell types such that efforts required for pharmaceutical development are minimized.

## SUMMARY OF THE INVENTION

**[0007]** In the present study, we used GeneChip (version U133A containing approximately 22,000 gene probes) to examine the cell type-selective transcriptome expression of 7 types of leukocytes (basophils, eosinophils, neutrophils, CD4<sup>+</sup> cells, CD8<sup>+</sup> cells, CD14<sup>+</sup> cells and CD19<sup>+</sup> cells), platelets, mast cells and fibroblasts by focusing on the expression of granulocyte-selective genes for ion channels, GPR and other receptors. We identified many novel granulocyte subtype-selective transcripts that are useful for drug development.

[0008] Granulocyte subtype selective transcripts were chosen based on several conditions such as the transcript having 5-fold or greater expression level compared to the maximum level of other leukocytes. Fifty-one transcripts were chosen to be preferentially expressed by each granulocyte subtype. Seventeen out of the 51 transcripts have not been previously reported as granulocyte subtype-selective. Among the 17 receptors and ion channels, six were basophil- and/or eosinophil-selective and were not highly expressed by other organs, indicating that they may be potential targets for anti-allergic drugs.

[0009] Utilization of this database (Attachment A) of potential cell type-selective drug targets will minimize the efforts required for pharmaceutical development of drugs for treatment of diseases of the immune system, cancer, cardiac diseases, as well as other diseases.

#### BRIEF DESCRIPTION OF THE DRAWINGS

[00010] Figure 1 shows Real-time quantitative PCR analysis of granulocyte-selective gene expression. The relative mRNA expression level by each cell type against PBMNC was shown after normalization of mRNA levels for *A.* HTm4 (0.42 per 100 GAPDH), *B.* Ca<sup>2+</sup> receptor alpha 1D subunit (0.003), *C.* prostaglandin E receptor type 3a2 (0.12), *D.* EMR-1 (0.62), and *E.* aquaporin 9 (0.92) expressed by PBMNC. Ne; neutrophils (*n*=3), Eo; eosinophils (*n*=2), Ba, basophils (*n*=3), CD4; CD4+ cells (*n*=3), P; PBMNC (*n*=1).

[00011] Figure 2 shows the demonstration of HTm4 protein on human basophils. Cells on the glass slide were incubated with 2 µg/ml polyclonal rabbit anti-hHTm4 antibody or 2 µg/ml rabbit IgG (H+L) as a control followed by incubation with a secondary antibody, highly cross-adsorbed Alexa Fluor® 546 conjugated goat anti-rabbit IgG (H+L) (Red). After mounting using the Prolong AntiFade Kit, slides were scanned by Zeiss Laser Scanning Microscope 5 Pascal.

[00012] Figures 3A through 3E shows granulocyte subtype-specific transcripts for ion channels and receptors.

[00013] Figures 4A through 4F show a table of “normalized AD” expression levels of various genes in indicated cells and shows corresponding graphs; x axis represents “normalized AD” expression levels.



**[00014]** Figures 5A through 5D show a table of “normalized AD” levels of various genes in indicated cells and shows corresponding graphs; x axis represents “normalized AD” expression levels.

**[00015]** Figures 6A through Figure 6R show the complete list of granulocyte subtype-selective transcripts.

#### DETAILED DESCRIPTION OF THE INVENTION

**[00016]** In this study, we have used high density oligonucleotide probe array (GeneChip) to measure the expression levels of approximately 20,000 different transcripts in highly purified cells. These cells were basophils, eosinophils, neutrophils, monocytes (CD14<sup>+</sup>), T lymphocytes (CD4<sup>+</sup> and CD8<sup>+</sup> cells), B lymphocytes (CD19<sup>+</sup>), lung-derived mast cells, cord blood-derived cultured mast cells, and nasal polyp-derived fibroblasts. The GeneChip assay allows the simultaneous measurement of large numbers of transcripts using relatively small numbers of cells. Using this technology, we could even measure triplicate transcriptome levels of basophils, the most rare granulocytes in peripheral blood.

**[00017]** Cell type-selective transcripts were selected based on the following criteria; (1) the average “normalized AD” expression level of each gene in a certain cell type must be 3-fold or greater than the maximal level in other cell types, and (2) must be significantly ( $p < 0.01$ ) greater than that in other cell types. (3) The “AD” expression level provided with “absence” or “marginal” call by GeneChip Suite Software should be observed only once or not at all in the three or four independent experiments (3 experiments for basophils, 4 experiments for eosinophils and neutrophils) using different cell populations performed. (4) For the transcripts preferentially expressed for the two different cell types such as basophils and eosinophils, the average “normalized AD” expression levels in the two cell types should be within 3-fold of each other. Using these standards, we found 83 basophil-selective, 37 eosinophil-selective, 257 neutrophil-selective, 34 basophil-eosinophil-selective, 19 eosinophil-neutrophil-selective, and 17 basophil-neutrophil-selective transcripts. Due to the functional similarity with basophils, mast cell-selective transcripts were also examined, and 63 mast cell-selective and 11 mast cell-basophil-selective transcripts were also detected (Table 1, and Figures 6A-6R). Since mast cells, basophils and eosinophils play similar roles in allergic inflammation, the transcripts preferentially expressed for the three granulocytes by comparing their average “normalized AD”

levels to other leukocytes. Thirty-four transcripts were then selected; however, most of them were overlapped with the transcripts listed in Figures 6A-6R. Only four transcripts (*MYB*, *SAMSN1*, *BACE2*, and *CASP3*) were found not overlapped, and they were not receptors or ion channels.

**[00018]** Among the 491 granulocyte-selective transcripts listed in Figures 6A-6R, 4 ion channels, 19 GPR and 28 other receptors were further selected (Figure 3). When plural transcripts obtained by different probe sets had identical Genebank or Unigene accession numbers (<http://www.ncbi.nlm.nih.gov/>), the transcript showing the highest expression level was selected.

*Ion channels and receptors preferentially expressed by granulocytes other than neutrophils*

**[00019]** Eosinophils, basophils and mast cells play an important role in the pathogenesis of allergic diseases, but do not play an essential role in killing microbes except for nematodes. On the other hand, neutrophils play a crucial role in killing microbes such as bacteria. Caution should be taken in regulating neutrophil function even in the case of neutrophil-induced inflammation. Therefore, the molecules present only in granulocytes except for neutrophils would be important pharmaceutical targets for allergic disorders.<sup>1,2</sup>

**[00020]** Among the 51 granulocyte-selective transcripts for ion channels and receptors, we identified 17 granulocyte-selective transcripts that have not been reported for their selective expression (shown in bold letters in Figure 3). Of these 17 transcripts, eight were preferentially expressed by granulocytes other than neutrophils. Among these eight transcripts, the two transcripts for fibroblast growth factor receptor 2 and low density lipoprotein receptor were found to be expressed by multiple tissue cell types (shown at the Web site [http://www.lsbm.org/index\\_e.html](http://www.lsbm.org/index_e.html)), which displays genomic expression of 55 different human tissue cells such as brain, heart and lung cells using the same experimental system. Affymetrix, U133A as ourts. Thus, they may not be suitable as a drug target because important organs that are unrelated to allergic inflammation (such as the brain) express it. Among the six novel transcripts found to be preferentially expressed by granulocytes except for neutrophils, we focus on the following four transcripts expressed by granulocytes including basophils. They were  $\text{Ca}^{2+}$  channel (*CACNA1D*), a prostaglandin E receptor, (*EP3A2*), epidermal growth factor-like module-containing mucin-like receptor (EMR) 1 (*EMR1*), and HTm4 (*MS4A3*).

**[00021]** Basophils are the rarest granulocytes present in human peripheral blood and as such their complete transcriptional profiles remain unclear and no basophil-selective transcripts have previously been reported.<sup>21</sup> Although eosinophils and mast cells have been considered as important therapeutic targets for allergic diseases for a long time, recent studies suggest the importance of basophils in pathogenesis of severe allergic diseases such as fatal asthma.<sup>2,22</sup> Therefore, we further examined the selective expression of these four basophil-, or basophil-eosinophil-selective transcripts by using real-time RT-PCR. As shown in the Fig. 1, including a known molecule preferentially expressed by neutrophils, aquaporin 9,<sup>23</sup> the results obtained with GeneChip assay were confirmed by using this highly accurate and reproducible method.<sup>24</sup>

**[00022]** Among these four molecules, we could obtain a suitable antibody against HTm4, which is a member of a family of four transmembrane- proteins which include CD 20 and high affinity Fc receptor for IgE (FcεRI) β-chain.<sup>25</sup> Genetics provided evidence for the existence of multiple loci relevant to atopic asthma on chromosome 11q13, including HTm4.<sup>26</sup> Most recently, we have published data identifying HTm4 as a hematopoietic cell cycle regulator.<sup>27</sup> Using specific antibody against HTm4, we could detect the expression of HTm4 at the protein level in basophils (Fig. 2). To confirm whether these ion channels and receptors could be potential drug targets for diseases involving basophil activation, the amount of molecules expressed by various cell types should be quantified and the effect of any identified antagonists should be tested on the cell types found to express these molecules.

**[00023]** As has been well documented and expected, Fc ε RI α, IL-3 receptors, IL-5 receptors, chemokine receptor CCR3,<sup>1,2</sup> sialic acid binding Ig-like lectin (Siglec)-8,<sup>28</sup> Siglec-6,<sup>15</sup> histamine H4 receptor<sup>29</sup> and chemoattractant receptor- homologous molecule expressed on Th2 cells (CRTH2)<sup>30</sup> were preferentially expressed by basophils and/or eosinophils or mast cells. These consistent observations strengthened the reliability of the present methods and research strategy. Indeed, the antibody against Siglec-8 can induce selective apoptosis of eosinophils, and is expected to be useful therapeutically.<sup>28</sup>

*Ion channels and receptors preferentially expressed by granulocytes including neutrophils*

**[00024]** Of the 17 transcripts that have not been reported as granulocyte-selective, nine were preferentially expressed by granulocytes including neutrophils. Pharmaceutical targets

of selective granulocyte transcripts should treat inflammatory diseases without affecting the function of important organs that are unrelated to inflammation as well as the function of lymphocytes. However, four of the nine neutrophil-selective transcripts were expressed by multiple organ tissues. One of the four neutrophil-selective transcripts encoded proteinase-activated receptor (PAR)-2, a receptor for mast cell tryptase, which is linked to the pathogenesis of allergic diseases such as asthma.<sup>31,32</sup> PAR-2 transcripts are also abundantly expressed by tissue types including skin and intestine which are often the target organs for allergic diseases. But the development of PAR-2 antagonists for use as anti-allergic drugs may be unsuitable because it may down regulate neutrophil function and thereby induce bacterial infection.

### *General discussion*

[00025] We identified 51 granulocyte-selective genes for ion channels and receptors by examining approximately 20,000 kinds of transcripts derived from 16,000 genes from 10 different types of cells using U133A GeneChip, which covers approximately half of the genes present in the human genome. The majority of these transcripts encoded molecules known or expected to be granulocyte subtype-selective such as the IL-3 receptor and Fc  $\epsilon$  receptors.

[00026] Mast cells expressed low levels of Fc  $\epsilon$  RI  $\alpha$  compared to basophils, and that even neutrophils expressed a substantial level of the receptor (Figure 3). This raises the possibility that GeneChip assay may not be suitable for detecting selective molecules. In the present study, however, only the GeneChip data obtained using cord blood-derived mast cells and lung mast cells could be employed due to the strict data selection based on the RNA quality (see Methods). As has been reported,<sup>14, 33</sup> peripheral blood-derived cultured mast cells or skin-derived mast cells expressed approximately 10-fold Fc  $\epsilon$  RI  $\alpha$  mRNA compared to cord blood-derived mast cells (data not shown). Also, as shown in Figures 6A-6R, only 2 of the 4 neutrophil samples expressed Fc  $\epsilon$  RI  $\alpha$  mRNA. This may be explained by the observation that only neutrophils obtained from some allergic donors express the molecule.<sup>34</sup>

[00027] We unexpectedly found 17 granulocyte-selective transcripts including HTm4. Basophil- and/or eosinophil-selective transcripts identified in our study could be potential therapeutic targets for allergic diseases because these granulocytes play a crucial role in allergic inflammation.<sup>1,2</sup> Granulocyte-selective transcripts could also be drug targets for other inflammatory diseases such as systemic vasculitis.<sup>3,4</sup> Analysis of cell type-selective transcripts

from database searches is expected to minimize the efforts required for drug discovery. The public database ([http://www.lsbm.org/index\\_e.html](http://www.lsbm.org/index_e.html)) shows that some granulocyte-selective transcripts (18 out of 51) detected in our study are abundantly expressed by multiple (more than 3) organ tissue cell types using the same GeneChip U133A probe array. Thus, the safety of any candidate drug must be evaluated by comparing its efficacy (on granulocytes) with its toxicity (to organs). Six out of the 17 novel granulocyte-selective molecules may be excluded from drug development due to their expression in multiple organs unrelated to the diseases. Thus, our approach has identified 11 receptors and ion channels with therapeutic potential. Especially, among the 11 receptors and ion channels, seven were basophil- and/or eosinophil-selective and were not expressed by other organs, indicating that they may be potential targets for anti-allergic drugs.

[00028] Finally, it should be stressed that basophils, the rarest leukocytes, have recently been found to play a more crucial role than we ever proposed in the pathogenesis of intractable allergic diseases such as fatal asthma.<sup>35,36</sup> Thus, targeting basophil receptors and ion channels such as HTm4 and Ca<sup>2+</sup> channel CACNA1D is particularly expected for the future drug discovery. The importance of molecules known to be expressed by basophils may be reevaluated regarding its selectivity. Freshly-isolated resting basophils expressed the highest level of IL-4 compared to other cell types. Because the basophil purification procedure requires more isolation steps, ex vivo manipulation may activate the cells. However, it should also be noted that basophils have been recently found as the major source of IL-4 at least in asthma models.<sup>37,38</sup>

## Materials and Methods

### *Purification of leukocytes*

[00029] All human subjects in this study provided written, informed consent, and the Ethical Review Boards at the relevant hospitals (National Center for Child Health and Development, and Jikei University School of Medicine) approved the study. The subjects used in this study were all healthy volunteers, especially having no allergic diseases.

[00030] Granulocytes and mononuclear cells were separated from venous blood of normal volunteers. Human basophils were semipurified by means of Percoll (Pharmacia, Uppsala, Sweden) density gradient centrifugation, and the cells were further purified by negative selection through use of a MACS Basophil Isolation Kit (Miltenyi BioTech, Bergisch-Gladbach,

Germany), as described previously.<sup>17</sup> Eosinophils were isolated by using Percoll (1.090 g/mL) density centrifugation. The eosinophils were further purified by negative selection with anti-CD16-bound micromagnetic beads, as described previously.<sup>18</sup> Neutrophils were isolated by using Percoll (1.085 g/mL) density centrifugation and further purified by negative selection using anti-CD81 antibody and antimouse IgG-bound micromagnetic beads to eliminate contaminating eosinophils. These granulocytes purified from human peripheral blood were spun down onto slide glass by Cytospin II (Shandon Southern Instruments, Inc., Sewickley, PA). The purity of these cells was evaluated based on 500 cells stained with May-Grünwald and Giemsa solutions.

**[00031]** For preparation of lymphocytes and monocytes, peripheral blood mononuclear cells (PBMNC) were isolated by centrifugation on lymphocyte separation medium (Organon Teknika Corp., Durham, NC). Monocytes (CD14<sup>+</sup> cells) were prepared using magnetic beads-conjugated CD14<sup>+</sup> antibody (CD14 MicroBeads; Miltenyi Biotec) from PBMNC. CD4<sup>+</sup> and CD8<sup>+</sup> cells were also respectively sorted using magnetic beads-conjugated CD4<sup>+</sup> (CD4 MicroBeads; Miltenyi Biotec) and CD8<sup>+</sup> antibodies (CD8 MicroBeads; Miltenyi Biotec) from PBMNC after depletion of CD14<sup>+</sup> cells with MACS CD14 MicroBeads (Miltenyi Biotec). The purity of CD4<sup>+</sup>, CD8<sup>+</sup> and CD14<sup>+</sup> cells was evaluated by staining the magnetic beads- conjugated cells compared to feasible control cell preparations such as unpurified cells with FITC-labeled goat anti-mouse Immunoglobulin (BD Pharmingen, Tokyo, Japan). Peripheral B cells were purified by a combination of negative (MicroBeads-conjugated antibodies to CD3, CD7, CD14, CD42b, and CD56; Miltenyi Biotec) and positive (CD19 MicroBeads; Miltenyi Biotec) selection using MicroBeads (Miltenyi Biotec). To obtain platelet rich plasma, blood samples were mixed with 3.8% (w/v) sodium citrate solution (9:1) and centrifuged at 260x g for 15 min. at 20°C. To remove any contaminating erythrocytes and leukocytes, the plasma was centrifuged again at 260x g for 15 min.

**[00032]** Human mast cells were derived from cord blood CD34<sup>+</sup> progenitor cells as described previously.<sup>11-14</sup> Briefly, progenitor cells purified from peripheral blood by CD34<sup>+</sup> isolation kits (Miltenyi Biotec), were cultured in Iscove's modified Dulbecco medium supplemented with 1% insulin-transferrin-selenium supplements (Life Technologies), 50 µM 2-mercaptoethanol, antibiotics, and 2% fetal calf serum in the presence of 100 ng/ml stem cell

factor and 50 ng/ml IL-6. After 11 to 14 weeks of culture, tryptase positive cells represented more than 99% of the cells.

*Purification of human lung mast cells and nasal polyp-derived fibroblasts*

[00033] Normal human lung tissue dissected during surgery was obtained macroscopically after informed consent. Human lung mast cells were dispersed from chopped lung specimens by an enzymatic procedure and were purified by magnetic bead affinity selection using the mAb anti-kit, YB5.B8 (BD PharMingen, San Diego, CA) as described previously.<sup>19</sup> The cells were further cultured in the presence of SCF and interleukin 6 (IL-6) for several weeks. Human nasal polyp-derived fibroblasts were obtained as previously reported.<sup>20</sup>

*GeneChip expression analysis*

[00034] Human genome-wide gene expression was examined using the Human Genome U133A probe array (GeneChip, Affymetrix, Santa Clara, CA), which contains the oligonucleotide probe set for 22,000 full-length genes. Experiments were performed in accordance with the manufacturer's protocol (Expression Analysis Technical Manual) and previous reports.<sup>11-14</sup> Total RNA (3–10 µg) was extracted from 10<sup>7</sup> cells. Double-stranded cDNA was synthesized using a SuperScript Choice system (Life Technologies) and a T7-(dT)24 primer (Amersham Pharmacia Biotech, Buckinghamshire, UK). The cDNA was subjected to *in vitro* transcription in the presence of biotinylated nucleoside triphosphates using a BioArray high-yield RNA transcript labeling kit (Enzo Diagnostics, Farmingdale, NY). The biotinylated cRNA was hybridized with a probe array for 16 h at 45°C. In some experiments as indicated in the supplementary table, biotinylated cRNA was prepared using two-cycles of cDNA synthesis and *in vitro* transcription for target amplification was performed according to the manufacturer's "The Small Sample Labeling Protocol version II" (Affymetrix, Inc). For the latter protocol, we employed 100 ng total RNA. After washing, the hybridized, biotinylated cRNA was stained with streptavidin-phycoerythrin (Molecular Probes, Eugene, OR) and then scanned with a HP gene array scanner. The fluorescence intensity of each probe was quantified using a computer program, GeneChip Analysis Suite 5.0 (Affymetrix). The expression level of single mRNA was determined as the average fluorescence intensity among the intensities obtained by 11 paired (perfect- matched and single nucleotide-mismatched) probes. If the intensities of mismatched

probes were very high, gene expression was judged to be absent, even if a high average fluorescence was obtained with the GeneChip Analysis Suite 5.0 program. The level of gene expression was determined as the average difference (AD) using the GeneChip software. Each AD level was then normalized by dividing it with the median value of 22,283 AD levels obtained in an experiment ("normalized AD" level).

*Real-time reverse transcriptase (RT)-PCR*

[00035] Total RNA was isolated using Isogen (Nippon gene, Tokyo, Japan) according to the manufacturer's instructions and quantified by measuring the absorbance at 260 nm. RNA was subsequently treated with DNase I (Life Technologies) reverse transcribed using Superscript II reverse transcriptase (Life Technologies). Real-time RT-PCR was performed 10 ng cDNA in 25 µl of final volume using the primers and probes supplied by "Assays-on-Demand Gene Expression system" (PE Applied Biosystem) according to the manufacturer's instructions. Measurement of gene expression was performed using the ABI PRISM 7700 Sequence Detector. The expression level of each gene was normalized to a GAPDH.

*Staining of basophils with anti-HTm4*

[00036] Basophils purified from human peripheral blood with Basophil Isolation Kit (Miltenyi Biotec) were spun down onto slide glass by Cytospin II (Shandon Southern Instruments Inc., Sewickley, PA). Cells were fixed with acetone for 1 minute and then blocked in goat serum in 50 mM TRIS-Cl, pH 7.4 for 1 hour. Cells were further incubated for 2 hours with 2 µg/ml of the polyclonal antibody rabbit anti-hHTm4. Cells were then washed three times with PBS and incubated with a secondary antibody, highly cross-adsorbed Alexa Fluor® 546-conjugated goat anti-rabbit IgG (H+L) (Red) (Molecular Probes, Eugene, OR) for one hour. After three PBS washes, air dried cells were further mounted using the Prolong Anti-Fade Kit (Molecular Probes, Eugene, OR). Slides were scanned by Zeiss Laser Scanning Microscope 5 Pascal (Carl Zeiss Microimaging Inc, Thornwood, NY).

*Purity and viability of the leukocytes, and RNA quality*

[00037] We used leukocyte samples in this study only if the purity of each cell type was at least 98%, but there are >0.5% contaminated cells in any of the samples. We could



not evaluate the purity of CD19<sup>+</sup> cells and platelets due to lack of feasible controls or methods. However, specific transcript markers for non-granulocytes (CD4, CD8, CD14, CD19, IgG, etc.) as well as granulocyte subtype-specific transcripts were reasonably expressed by each leukocyte type as shown in Figures 6A-6R. Regarding the viability, we qualified the RNA before GeneChip assay using Array Quality Metrics Comparisons Software (Affymetrix) as well as trypan blue staining (they were always >95% viable), since RNase-rich granules derived from degenerating cells rapidly destroy RNA transcripts. Briefly, to evaluate the quality of RNA, the ratio of 3'-probe set and 5'-probe set of housekeeping genes were compared as shown in Figures 6A-6R. According to the above software's guidance, the ratio of >2:1 at standard sample (5µg total RNA) protocol and that of >10:1 at small sample (50 ng total RNA) protocol were recommended. As shown in Figures 6A-6R, the cells used in the present study had the appropriate ratios of 3'-probe set and 5'-probe set of housekeeping genes, suggesting that these cells were highly viable.

#### *Statistical analysis*

**[00038]** Since logarithmic “normalized AD” levels were normally distributed within each group, unpaired parametric Student’s two-tailed *t*-test was employed to analyze the data on a logarithmic scale.

Table 1. Representative cell type-selective transcripts in granulocytes

Accession # <sup>a</sup>	Transcript	S.I. <sup>b</sup>	Normalized AD level
<i>Basophil-selective</i>			
NM_000589.1	IL-4	73.3	13.3
L35848.1	HTm4	38.2	132.1
BC005912.1	Fc $\epsilon$ RI $\alpha$	12.7	218.9
<i>Eosinophil-selective</i>			
NM_001140.1	Arachidonate 15-lipoxygenase	74.1	18.3
NM_024703.1	FLJ22593	19.1	29.1
NM_014442.1	Siglec-8	9.8	16.9
<i>Neutrophil-selective</i>			
NM_004633.1	IL-1 R, type II	127.9	51.5
U73191.1	inward rectifier K <sup>+</sup> channel Kir1.3	107.5	98
NM_001557.1	CXCR2 (IL-8 receptor $\beta$ )	39.3	105.2
<i>Mast cell-selective</i>			
AF206667.1	tryptase $\beta$	84.3	159.4
NM_001911.1	cathepsin G	51.5	72.1
BC005929.1	major basic protein	31.6	72.5
<i>Basophil-eosinophil-selective</i>			
M75914.1	IL-5R $\alpha$	42.8	19.4(B), 29.3(E)
NM_004778.1	CRT2	16.6	23.9(B), 38.1(E)
NM_001828.3	Charcot-Leyden crystal protein	15.2	229.2(B), 198.6(E)
<i>Eosinophil-neutrophil-selective</i>			
NM_005306.1	GPR 43 (PAR1-like)	21.7	11.7(E), 32.9(N)
NM_004668.1	DHHC domain containing 18	6.6	16.2(E), 44.5(N)
<i>Basophil-neutrophil-selective</i>			
NM_016006.1	CGI-58 protein	5.8	12.6(B), 21.2(N)
<i>Basophil-mast cell-selective</i>			
NM_001870.1	carboxypeptidase A3	59.2	111.7(M), 137.3(B)
NM_002529.2	TRK neurotrophin receptor	34.7	3.1(M), 7 (B)
NM_000139.1	Fc $\epsilon$ RI $\beta$	21.2	22.2(M), 43.8(B)

a. The GenBank accession number (<http://www.ncbi.nlm.nih.gov>).

b. Selectivity index (S.I.) was calculated by comparing the “normalized AD” level in a cell type or of two cell types with the maximal gene expression level of the other 8 or 9 cell types. The complete list of the genes having >3 S.I. is shown in Supplementary Table 1.

**[00039]** Figures 6A-6R show the complete list of granulocyte subtype-selective transcripts. Selectivity index (S.I.) was calculated by comparing the “normalized AD” level of a cell type or of two cell types with the maximal gene expression level of the other 8 or 9 cell types including platelets (Pl), CD4<sup>+</sup> cells (CD4), CD8<sup>+</sup> cells (CD8), CD14<sup>+</sup> cells (CD14), CD19<sup>+</sup> cells (CD19) and nasal polyp-derived cultured fibroblasts (Fb). Transcripts having S.I. >3-fold were shown in Figures 6A-6R A-H. *A.* Basophil (Ba)-selective transcripts. *B.* Eosinophil (Eo)-selective transcripts. *C.* Neutrophil (Ne)-selective transcripts. *D.* Mast cell (MC)-selective transcripts. *E.* Basophil and eosinophil-selective transcripts. *F.* Eosinophil and neutrophil-selective transcripts. *G.* Basophil and neutrophil-selective transcripts. *H.* Mast cell and basophil-selective transcripts. *I.* Raw AD levels for the median values used to normalize the raw AD levels, and the housekeeping genes. When the result was accompanied by presence call, it was shown as a bold numeral. Italic numerals show that the raw AD levels were associated with absence call by the GeneChip analysis software. 1. Abbreviations used in the tables were (small); the results obtained by the small sample protocol (see materials and methods), R; receptor, and ICN; ion channel.

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**[00040]** The references cited herein are incorporated by reference.

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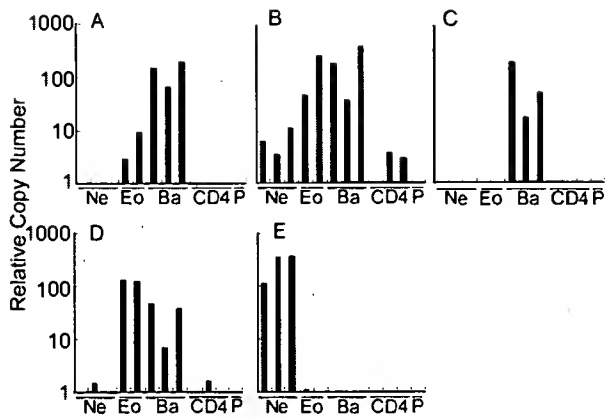
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Figure 1





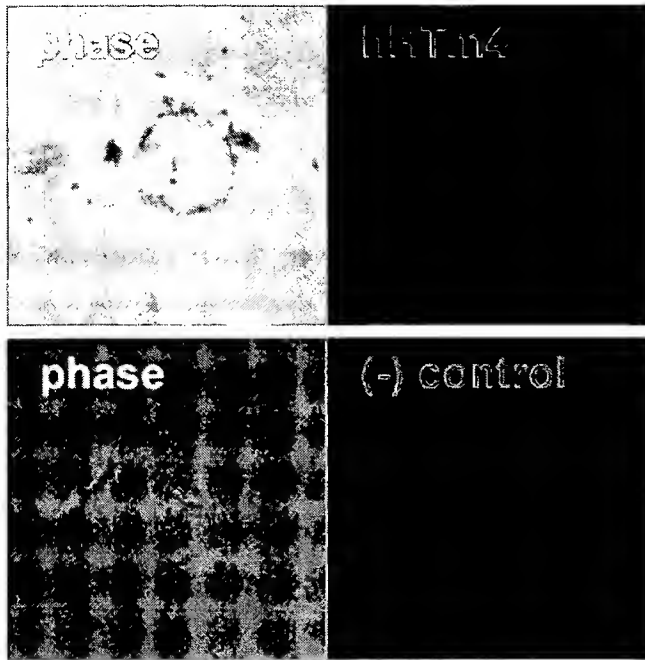


Figure 2

Figure 3A

Figure 3. Granulocyte subtype-specific transcripts for ion channels and receptors

<i>Ion Channels</i>												<i>Gene Functions</i>	
Transcript (Accession #, GenBank)	Cell-type*	MC	Ba	Eo	Ne	PI	CD4	CD8	CD14	CD19	Fb	TC*	
<u>Ca<sup>2+</sup> channel type A1 D (BE550599)</u>	Ba, Eo	0.1	1.7	1.5	0.4	0.0	0.3	0.1	0.0	0.3	0.0	0	facilitates uptake of the metalloids arsenite and antimonite
<u>aquaporin 9 (NM_020980) 602914</u>	Ne	0.7	0.1	0.4	137.4	0.4	0.9	0.1	8.6	0.1	0.2	7	
<u>K<sup>+</sup> channel Kir1.3 (U73191) 600359</u>	Ne	0.9	0.2	0.4	99.5	0.7	0.2	0.0	0.8	0.0	0.0	5	
<u>K<sup>+</sup> channel Kir2.1 (AF153820) 600681</u>	Ne	0.7	3.8	5.3	40.7	0.4	0.2	0.5	1.5	0.7	1.1	6	Andersen syndrome (170390) and Bartter syndrome (241200)
<u>GPCR</u>													Andersen syndrome (170390) and Bartter syndrome (241200) and Bartter syndrome (241200)
<u>histamine H<sub>4</sub> R (AF312230) 606792</u>	Ba	0.7	34.2	9.4	0.7	0.4	0.8	0.5	0.6	0.0	0.1	0	expression of HRH4 conferred sensitivity
<u>PGC<sup>α</sup> R type 3a2 (X83858) 176806</u>	Ba	0.8	10.3	0.1	0.7	0.6	0.3	0.2	0.2	0.5	1.7	0	signaling pathways
<u>C3a R (U62027) 605246</u>	Ba, Eo	11.8	55.7	39.4	2.0	1.6	1.6	1.5	3.0	0.6	0.5	3	anaphylatoxin receptor
<u>CCR3 (NM_001837) 601268</u>	Ba, Eo	0.6	117.4	90.9	24.9	0.2	0.5	0.4	0.2	0.2	0.4	0	importance for eosinophil responses
<u>CRTH2 (NM_004778) 604837</u>	Ba, Eo	1.1	26.0	38.2	2.0	0.8	1.4	1.0	1.2	0.9	0.5	0	mediate signals to the interior of the cell via activation of heterotrimeric G proteins
<u>EMR-1 (NM_001974) 600493</u>	Ba, Eo	0.8	33.5	90.9	4.2	3.4	1.7	0.8	7.1	1.6	0.5	1	Probably involved in cellular response to a hormone
<u>adenosine A<sub>1</sub> R (NM_000677) 600445</u>	Eo	2.6	2.9	15.4	2.3	1.2	1.6	0.5	2.0	0.5	0.5	0	cardioprotective function
<u>P2Y2 purinergic R (NM_002564) 600041</u>	Eo	0.1	0.1	5.5	0.1	0.2	0.1	0.3	1.2	0.2	0.1	0	P2RY2 may participate in control of the cell cycle of endometrial carcinoma cells
<u>GPR105 purinergic R (NM_014879)</u>	Eo	2.6	2.9	15.4	2.3	1.2	1.6	0.5	2.0	0.5	0.5	2	GPR105 is a G-protein-coupled receptor identifying a quiescent, primitive population of hematopoietic cells restricted to bone marrow; GPR105 might play an important role in peripheral and neuroimmune function
<u>GPR, Edg-4 (AF011466) 605110</u>	Eo, Ne	1.3	2.8	15.9	24.2	0.1	3.6	5.0	3.8	1.9	0.9	2	ed-4 mma was expressed in mouse islets; <u>edg-4 (tpa2)</u> is a distinctive functional marker for ovarian carcinoma, and is expressed both as the wild-type and a carboxyl-terminally extended gain-of-function mutant
<u>PARI-like GPR43 (NM_005306)</u>	Eo, Ne	0.3	0.7	12.4	35.2	0.8	0.1	0.1	0.7	0.4	0.1	0	the highest levels of gpr43 were

**Figure 3B**

[illegible]

Figure 3C

formyl peptide R 2 ( <u>U81501</u> )											
Ne	0.4	0.5	0.6	75.5	0.1	1.0	0.6	6.0	0.8	0.1	5
GPR77 ( <u>NM_018485</u> )											
Ne	0.1	0.9	0.8	3.4	0.0	0.3	0.2	1.0	0.1	0.3	2
GPR86 purinergic R ( <u>NM_023914</u> )											
Ne	0.3	0.2	17.9	88.2	1.9	0.1	0.2	12.3	0.6	0.0	1
PAR2 ( <u>BE965369</u> ) <u>600933</u>											
Ne	0.1	0.3	2.2	36.2	0.1	0.7	0.1	1.6	0.4	1.2	15
<i>Other Receptors</i>											
Ba	19.4	219.0	4.6	5.5	1.4	5.1	0.8	1.4	0.4	0.2	0
Ba	0.6	133.1	6.9	3.5	0.2	0.5	0.4	0.1	0.2	0.0	1
Ba	0.6	52.6	2.0	0.7	0.2	0.3	0.2	0.7	0.1	0.1	0
Ba, Eo	0.3	56.0	16.5	1.2	0.1	0.4	3.5	5.2	1.1	0.1	0
<u>CD244NKcellR</u> ( <u>NM_016382</u> ) <u>605554</u>											
Ba, Eo	0.1	27.9	12.1	0.2	0.1	0.1	0.2	0.1	0.1	1.0	17
Ba, Eo	0.9	20.5	30.4	0.6	0.1	0.1	0.1	0.1	0.2	0.1	0
Eo	1.8	0.3	17.4	0.4	0.3	0.2	0.1	0.2	0.5	0.2	0
CD117 c-KIT ( <u>NM_000222</u> ) <u>164970</u>											
MC	89.0	7.2	4.2	1.2	0.8	0.2	0.5	0.1	0.1	0.5	15
<u>Siglec 6</u> ( <u>D86358</u> ) <u>604405</u>											
MC	5.6	0.2	0.0	0.2	0.5	0.0	0.0	0.0	0.4	0.0	0
MC, Ba	22.3	44.3	0.4	0.6	1.6	0.5	0.2	0.0	0.3	0.1	0
MC, Ba	20.7	20.4	1.3	1.8	2.3	2.1	3.4	3.5	0.8	6.3	34

VIA A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM. likely FPR2, mediates superoxide production at high concentrations of FMLF. C5L2 is an anaphylatoxin-binding protein with unique ligand binding and signaling properties. GPR86 proved to be a G(i)-coupled receptor displaying a high affinity for ADP, similar to the P2Y(12) receptor and can therefore be tentatively called P2Y(13). PAR2 plays a key role in chronic joint inflammation. responsible for initiating the allergic response. Cell cycle regulator. promotes the proliferation and differentiation of hematopoietic cells. engagement of 2B4 with specific antibody activates NK cytolytic activity. Receptor for acidic and basic fibroblast growth factors. lacking either IL5ra or Sox4 have defects in B-cell development. SIGLEC8 expression on eosinophils but not other leukocytes. Signaling from the KIT receptor tyrosine kinase is essential for primordial germ cell growth both in vivo and in vitro. OBBP1 is almost exclusively expressed on B cells. MS4A2 Allergic disease. receptor-mediated endocytosis

Figure 3 D

(NM_000527) 606945 TRK neurotrophin R (NM_002529) 191315	MC, Ba	4.6	7.3	0.1	0.1	0.1	0.1	0.1	0.1	0.0	0.0	0	participates in the primary signal transduction mechanism of NGF; is also an immunoregulatory cytokine acting on monocytes
butyrophilin like R (AK025267)	Ne	1.1	1.7	1.5	1.5	1.7	1.6	0.9	1.5	1.3	1.3	1	his gene is mainly expressed in small intestine, colon, testis, and leukocytes
CD120a, TNF-R-1 (NM_001065) 191190	Ne	1.7	1.2	7.8	74.7	1.3	2.2	5.9	17.4	0.6	16	35	Receptor for TNFSF2/TNF-alpha and homotrimeric TNFSF1/lymphotoxin-alpha
													The adaptor molecule FADD recruits caspase-8 to the activated receptor. The resulting death-inducing signaling complex (DISC) performs caspase-8 proteolytic activation which initiates the subsequent cascade of caspases (aspartate-specific cysteine proteases) mediating apoptosis. Contributes to the induction of noncytotoxic TNF effects including anti-viral state and activation of the acid sphingomyelinase.
CD95, Fas, APO-1 (AA164751) 134637	Ne	1.4	10.9	7.3	50.4	1.3	5.6	4.8	3.6	2.6	9.7	7	Receptor for TNFSF6/FASL. The adaptor molecule FADD recruits caspase-8 to the activated receptor. The resulting death-inducing signaling complex (DISC) performs caspase-8 proteolytic activation which initiates the subsequent cascade of caspases (aspartate-specific cysteine proteases) mediating apoptosis. FAS-mediated apoptosis may have a role in the induction of peripheral tolerance, in the antigen-stimulated suicide of mature T-cells, or both. The secreted

Figure 3 E

decoy R 1, TRAILR3 (AF012536) 603613	Ne	0.1	1.5	7.7	78.7	0.5	0.2	0.1	0.7	0.1	0.6	0	isoforms 2 to 6 block apoptosis (in vitro), does not induce apoptosis.
Fcγ R IIc2 (U90939)	Ne	1.5	2.4	7.8	59.9	0.3	0.2	0.1	7.2	2.3	0.2	2	
Fcγ R IIc3 (U90940)	Ne	2.4	10.7	10.0	84.3	3.0	1.4	0.6	14.0	7.2	1.0	5	
Fcγ R III (J04162) 146740	Ne	0.7	1.6	1.9	199.6	6.6	1.3	1.3	2.2	2.6	0.1	4	failure of the patient's neutrophils to express Fc receptor III was associated with SLE
G-CSF R (NM_000760) 138971	Ne	0.1	0.4	1.6	163.6	0.2	0.8	0.2	25.5	0.1	0.2	3	inhibits cell proliferation and survival in response to CSF3
IL-13 R (U81379) 308385	Ne	0.3	0.2	2.0	14.1	0.4	0.4	0.3	2.9	1.3	1.3	0	promotes the proliferation and differentiation of hematopoietic cells
IL-1R, type II (NM_004633) 147811	Ne	0.1	0.1	0.1	53.5	0.2	0.4	0.1	0.2	0.0	0.0	3	type II receptor inhibits IL1 activity by acting as a decoy target for IL1
IGFR 1 (NM_000875) 147370	Ne	0.3	3.5	5.0	17.4	1.6	0.1	2.8	2.4	2.0	3.5	3	IGFs may elicit a myogenic event which may be a key mechanism in the etiology of breast and ovarian cancer
IGFR 2 (NM_000876) 147280	Ne	4.6	0.9	5.4	85.3	1.7	2.9	8.7	8.4	4.8	15	32	Mutation in either MPRD or MPRI might result in a clinical disorder resembling a mucopolidosis
leukocyte immunoglobulin-like R A2 (NM_006866) 604812	Ne	0.5	5.8	4.3	41.2	1.8	0.0	0.1	11.6	0.5	0.1	2	Eosinophils may be activated through LIR7 for release of eosinophil-derived neurotoxin
Toll-like R 1 (AL050262) 601194	Ne	0.6	0.3	1.2	31.5	1.6	0.8	0.7	3.0	1.5	0.3	0	that TLR2-TLR1 heterodimers mediated the strongest cell activation
Toll-like R 2 (NM_003264) 603028	Ne	0.9	6.0	1.3	83.8	1.6	1.3	0.1	26.3	0.9	0.4	0	TLR2 is a molecular link between microbial products, apoptosis, and host defense mechanisms
Toll-like R 6 (NM_006068)	Ne	0.5	1.0	0.9	8.8	0.1	0.9	0.9	2.1	1.2	0.6	0	immunostimulatory activity

a. Cell-type specificity was obtained by comparing the "normalized AD" levels of each gene in mast cells (MC; average of 2 experiments), basophils (Ba; average of 3 experiments), eosinophils (Eo; average of 4 experiments), neutrophils (Ne; average of 4 experiments), platelets (Pl), CD4<sup>+</sup> cells (CD4), CD8<sup>+</sup> cells (CD8), CD14<sup>+</sup> cells (CD14), CD19<sup>+</sup> cells (CD19) and nasal polyp-derived cultured fibroblasts (Fb).

	CB cultured		cultured		MCs		Basophils		basophils		Eosinophils		Neutrophils		platelets		Erythrocytes		CD4		CD8		CD14		CD19	
Spink5					21	17	11	11	22	16	30	15	28	36	129	104										
chymase human					1221	47	65	65	45	12	101	62	108	59	104	45										
tryptase alpha					21179	212	40	40	33	25	184	139	104	17	52	39										
tryptase beta					25414	195	113	113	49	28	152	10	122	113	93	6										
tryptase delta					349	45	6	6	23	55	74	113	11	10	42	11										
tryptase gamma					654	56	19	19	38	78	28	24	81	230	142	83										
TRPV2					129	37	15	15	97	99	259	137	133	67	97	110										
ANKTM1					28	28	8	8	38	30	96	18	14	46	11	28										
Cannabinoid receptor type 1					50	41	14	14	47	36	27	61	41	56	18	54										
Cannabinoid receptor type 2					160	369	226	226	578	177	271	530	324	232	212	421										

Figure 4A

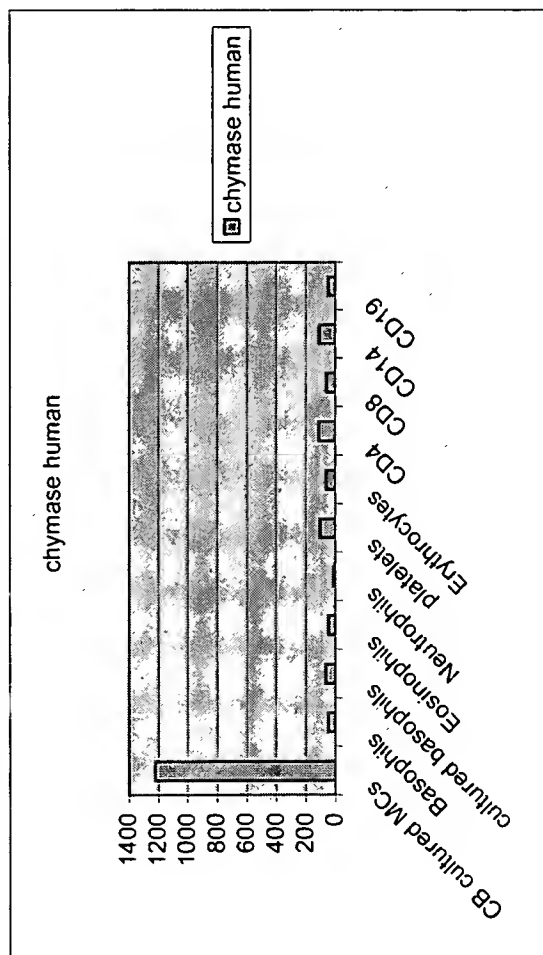
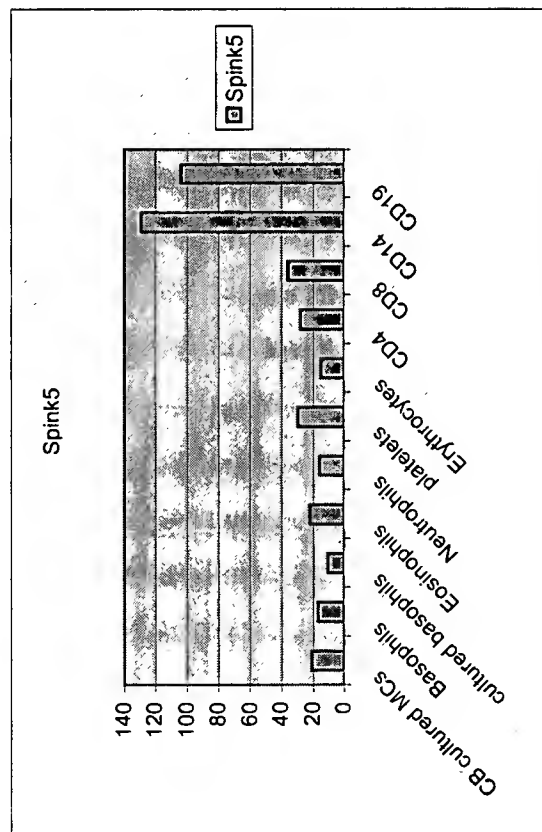


Figure 4B



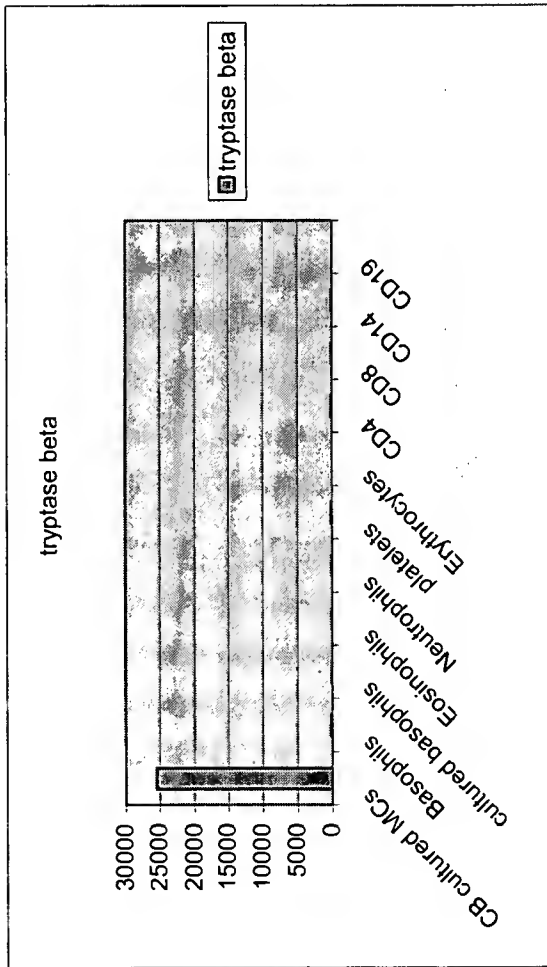
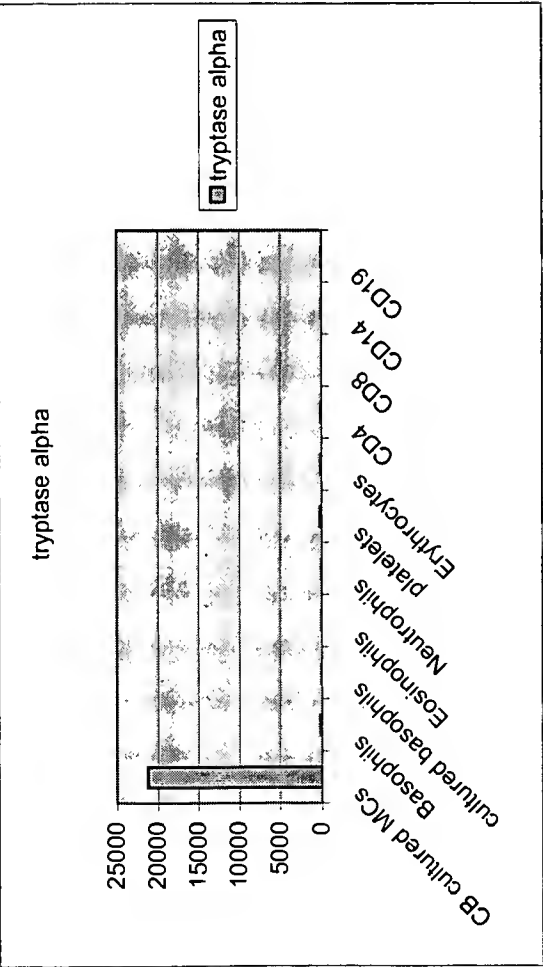


Figure 1c

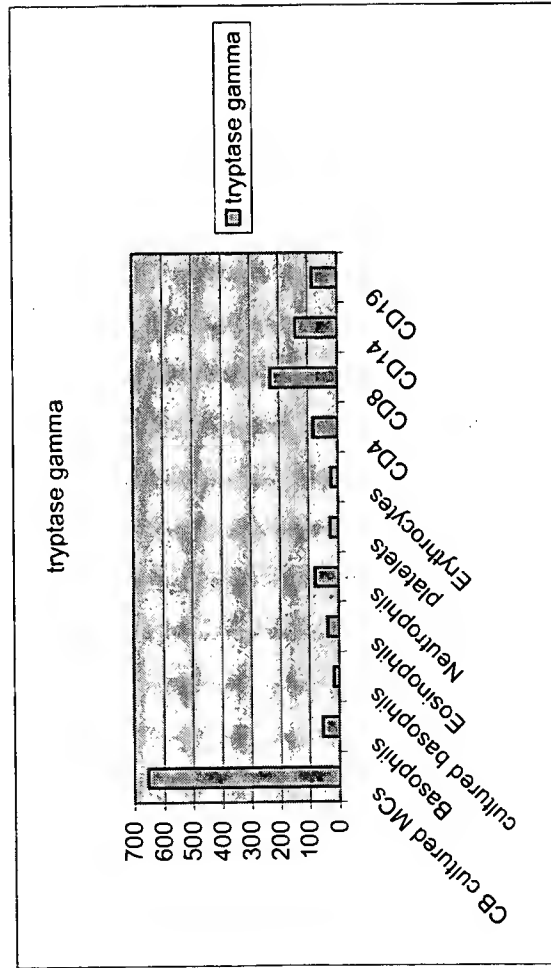
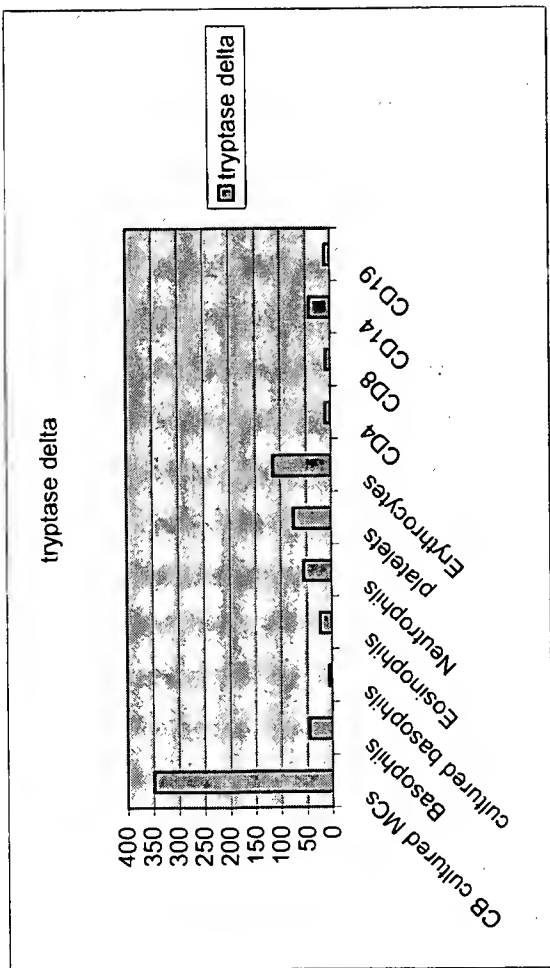


Figure 4 D

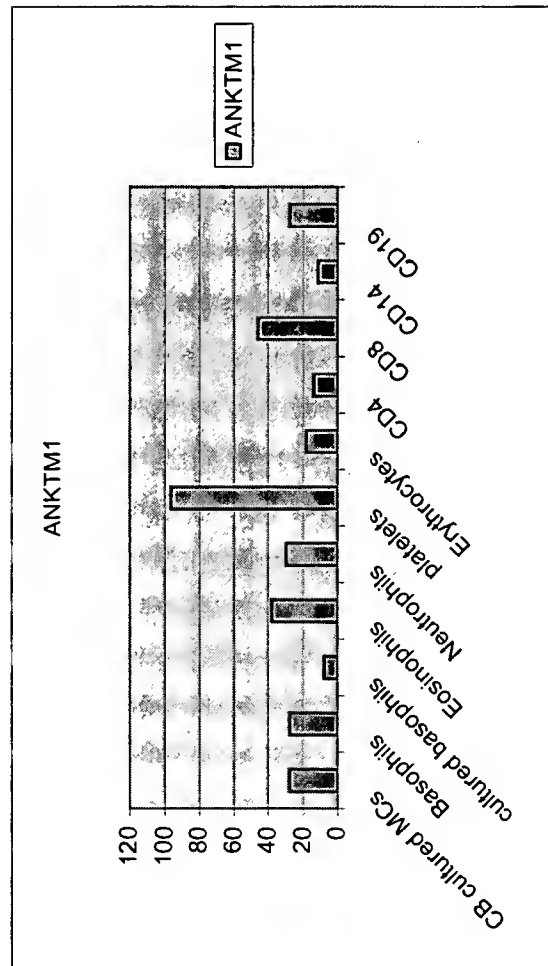
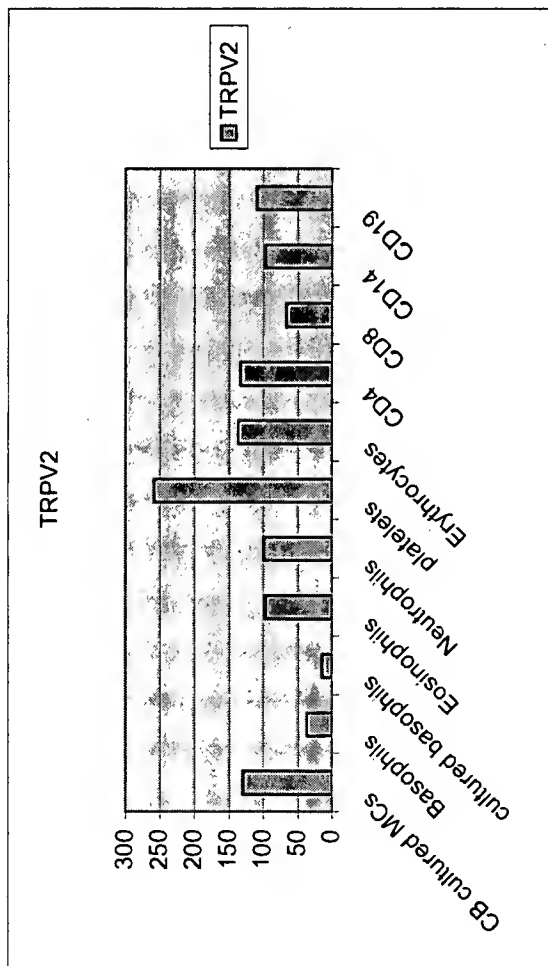


Figure 4E

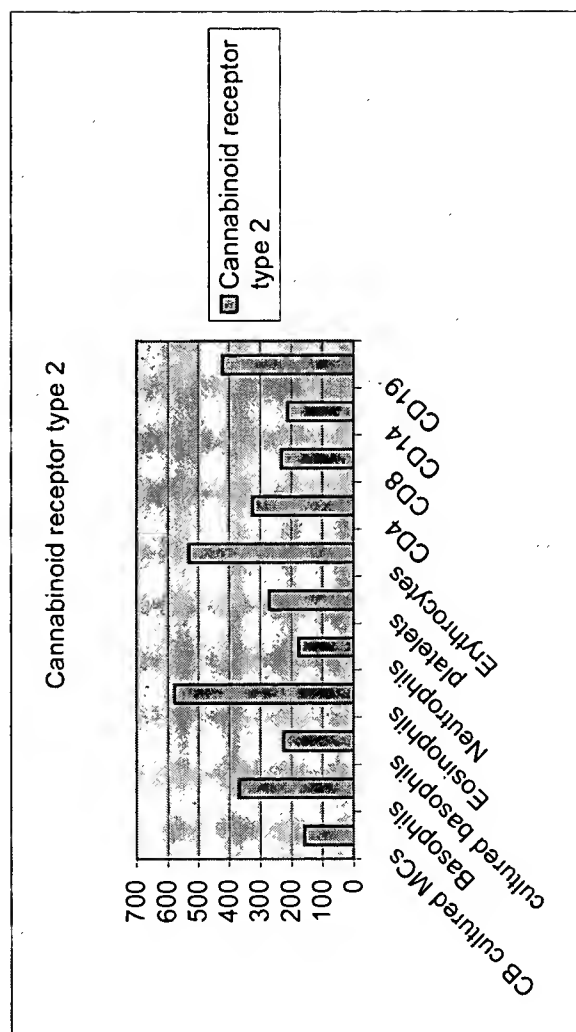
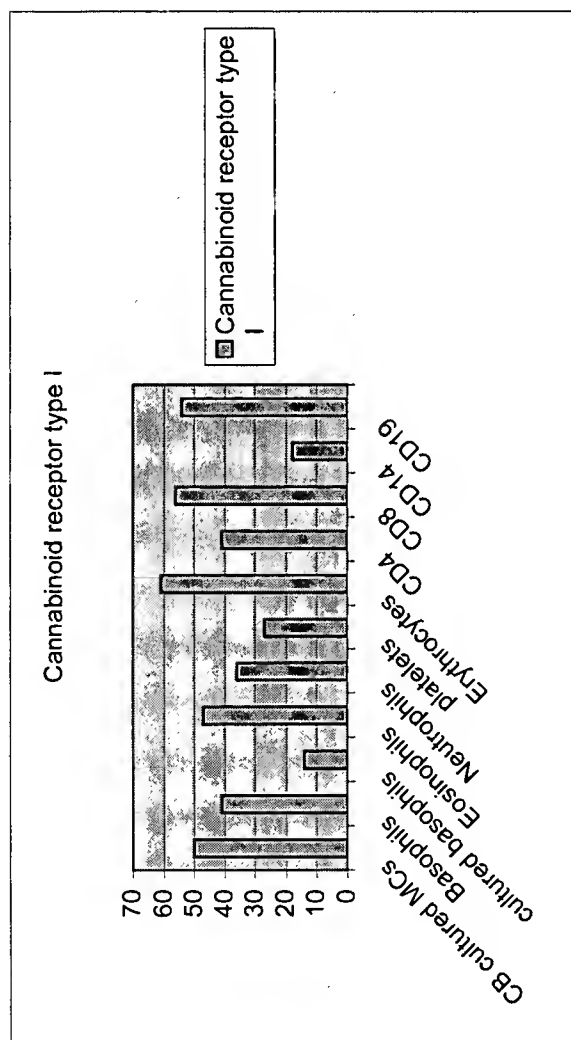


Figure 4j

	CB cultured		cultured basophils	Eosinophils	Neutrophils	platelets	Erythrocytes	CD4	CD8	CD14	CD19
	MCs	Basophils									
LILRB5	86	28	39	26	37	125	46	103	95	85	28
LILRA3	4	45	1004	59	84	18	68	31	68	451	13
LILRB1	165	84	51	258	1261	31	42	13	18	1105	125
LILRB2	375	780	227	1755	4237	199	375	286	58	2963	214
LILRA2	49	614	384	461	3269	146	318	8	9	1247	52
LILRA1	28	50	45	154	389	120	148	127	35	539	86
KIR3DL2	7	58	34	18	23	13	106	14	286	68	204
KIR2DS3	22	17	21	27	28	35	11	28	110	88	111
KIR2DL3 variant	30	54	134	66	61	149	95	39	247	147	271
KIR2DS1	35	138	81	88	93	191	132	57	257	21	267
KIR2DS5	24	31	23	21	21	53	27	33	135	19	173
KIR2DL4	139	140	85	157	144	280	210	35	239	152	196
KIR2DL4	11	45	41	50	41	88	15	19	72	77	85
KIR-123FM	41	43	31	20	52	31	121	96	163	26	193
KIR2DL5.3	27	83	24	41	49	61	239	92	323	56	72
KIR3DL1	68	89	41	51	95	75	97	76	169	36	196
MIR cl-10	144	621	83	1334	2386	107	146	145	52	2154	99
PTPRF	18	14	5	28	37	86	12	13	14	32	23

Figure 5A

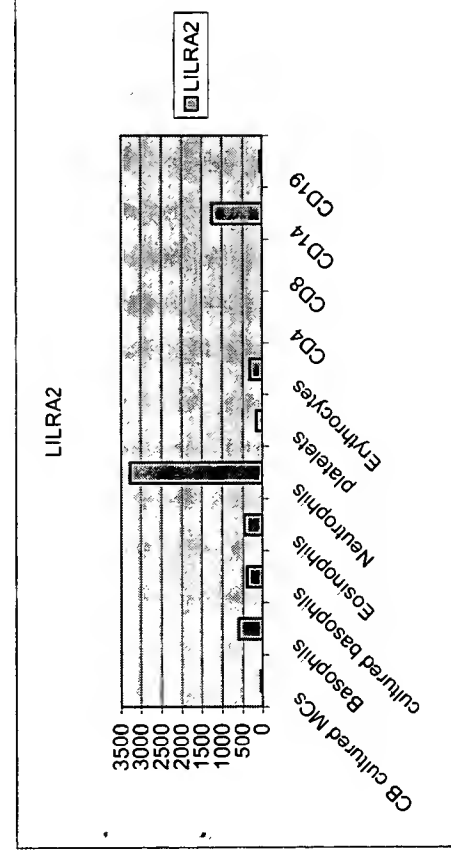
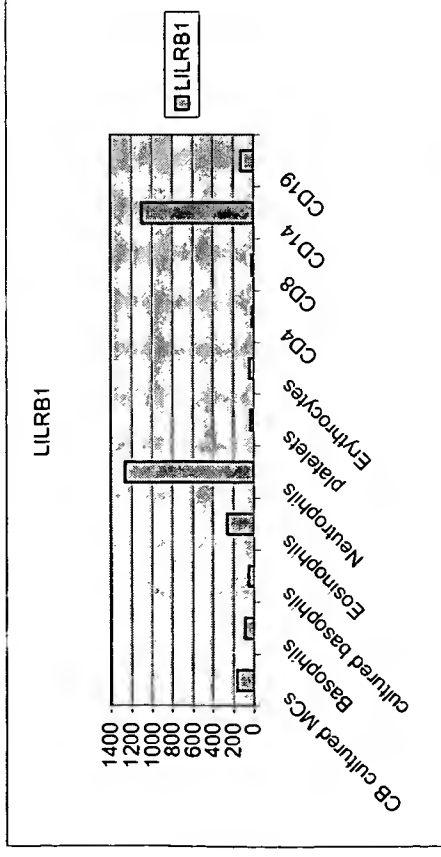
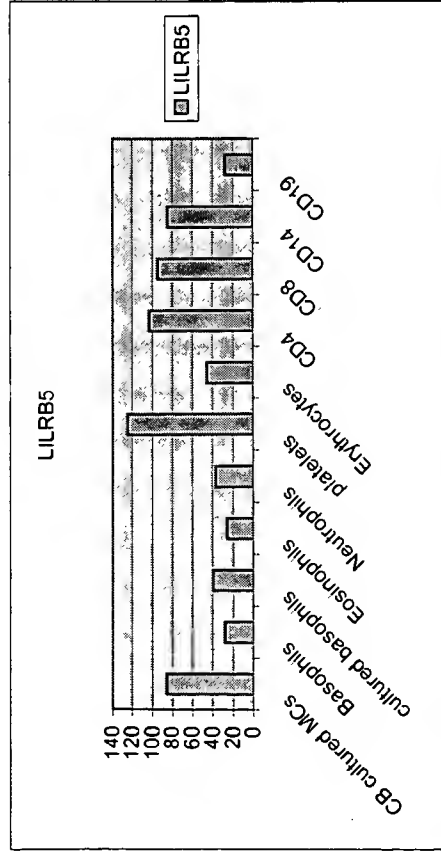
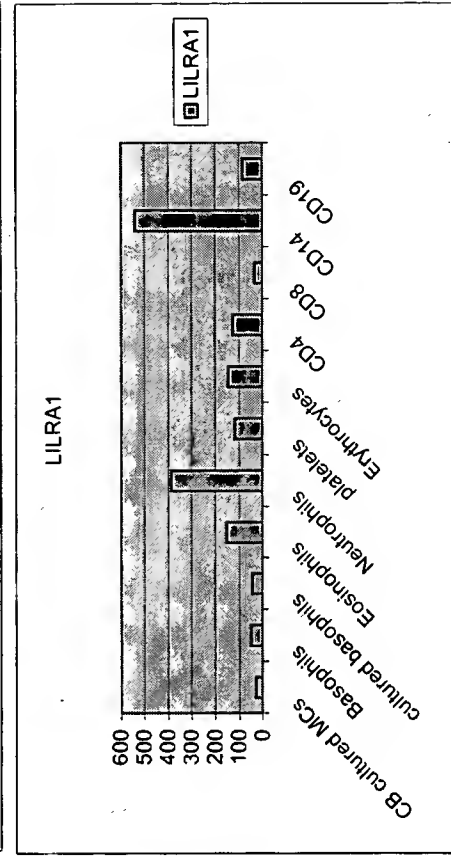
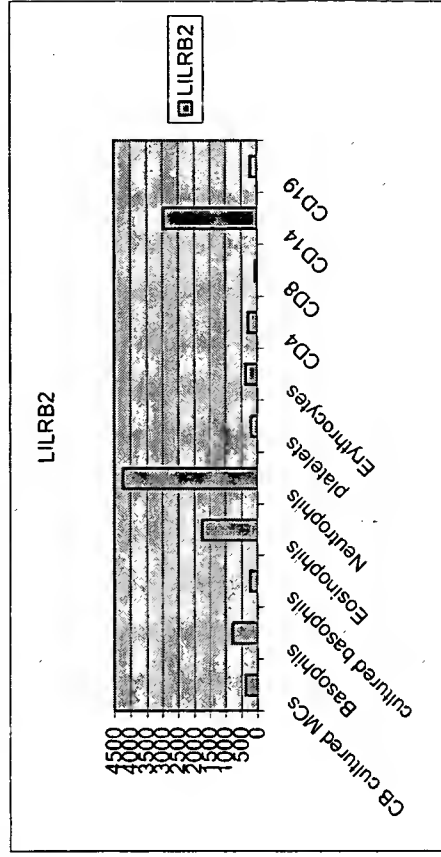
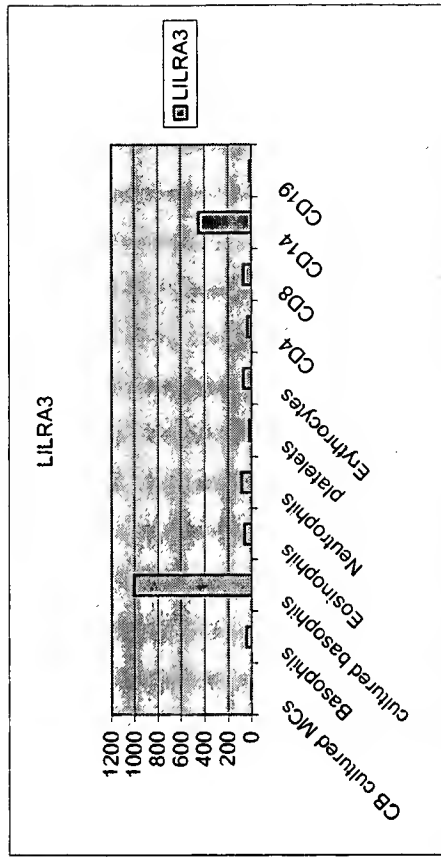


Figure S3

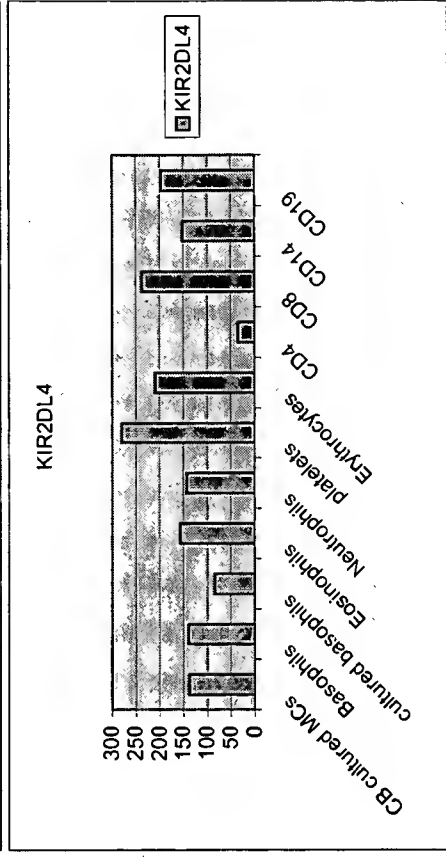
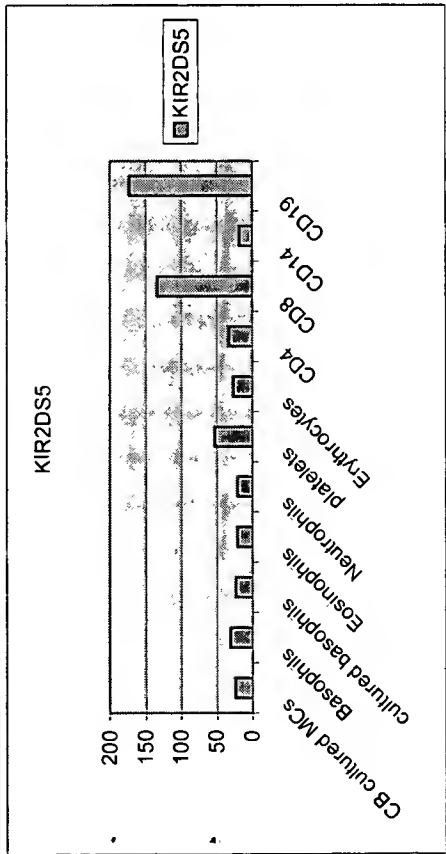
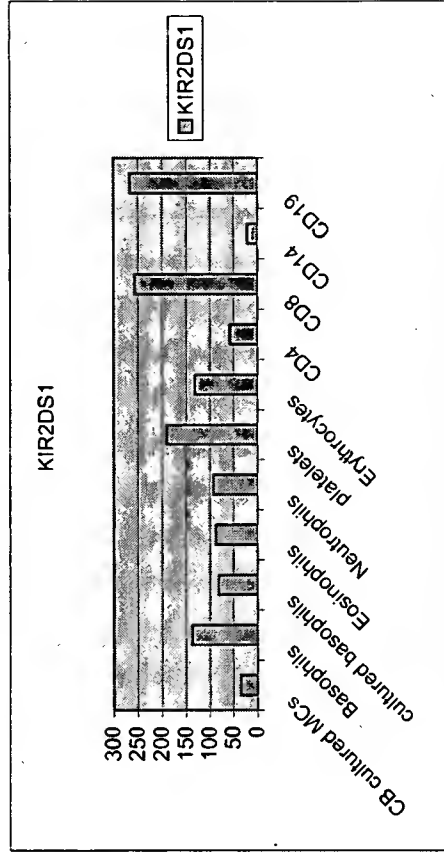
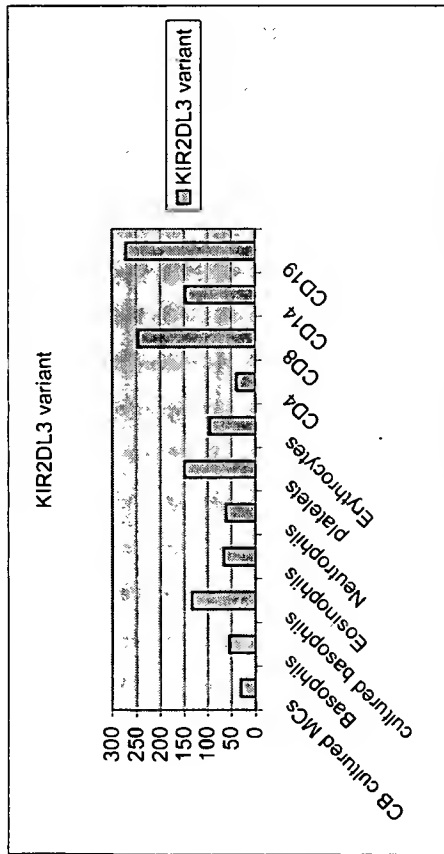
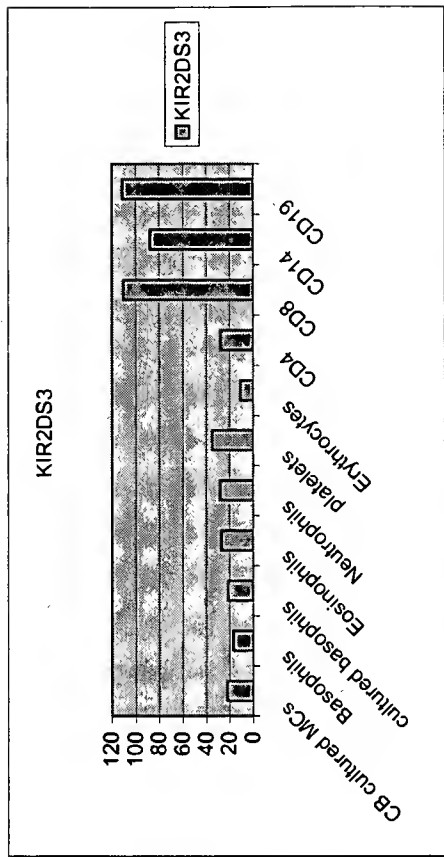
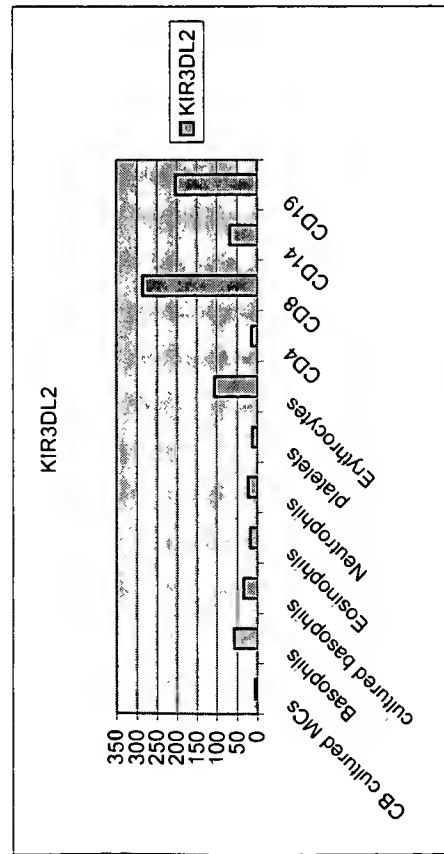


Figure 5C

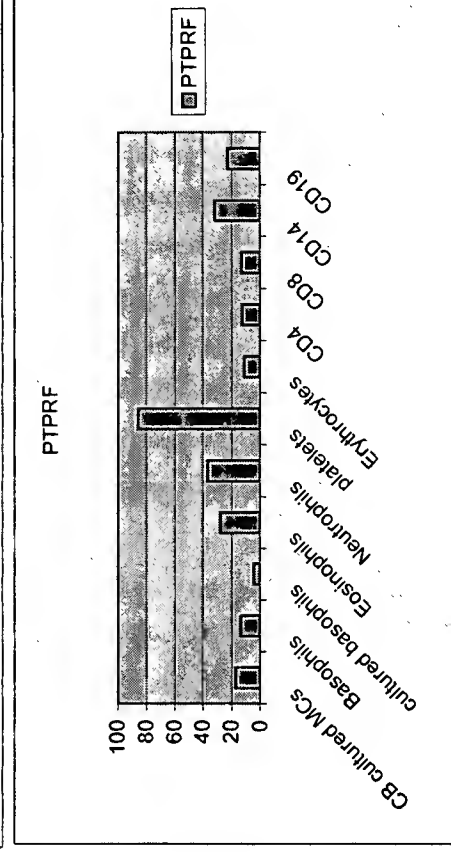
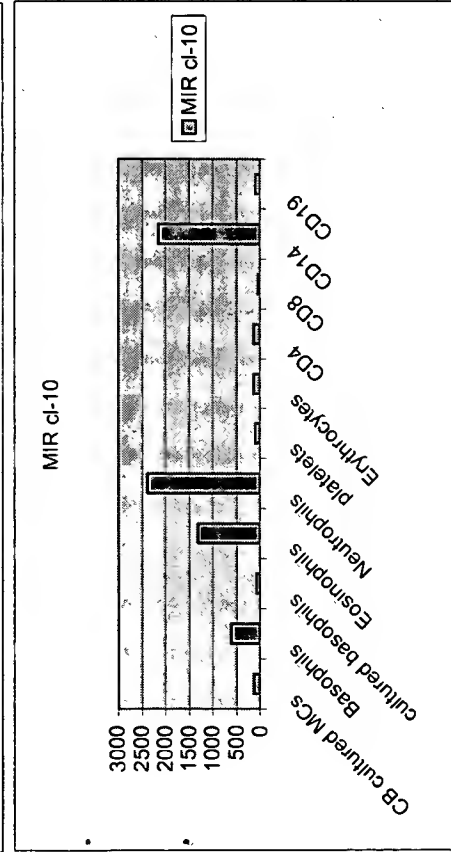
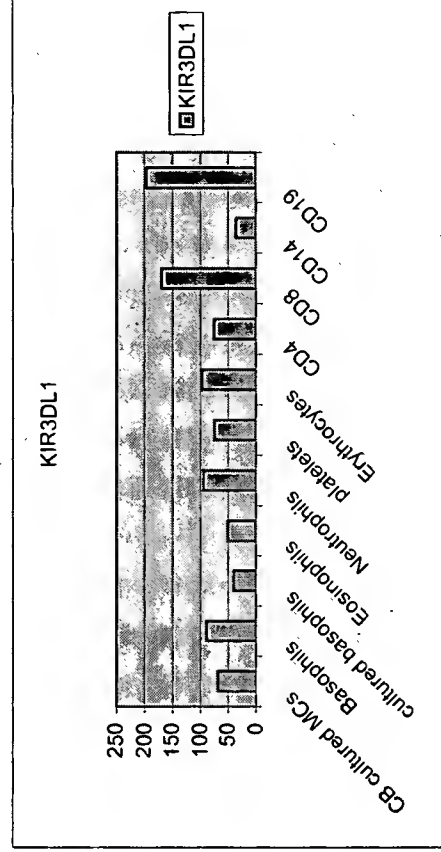
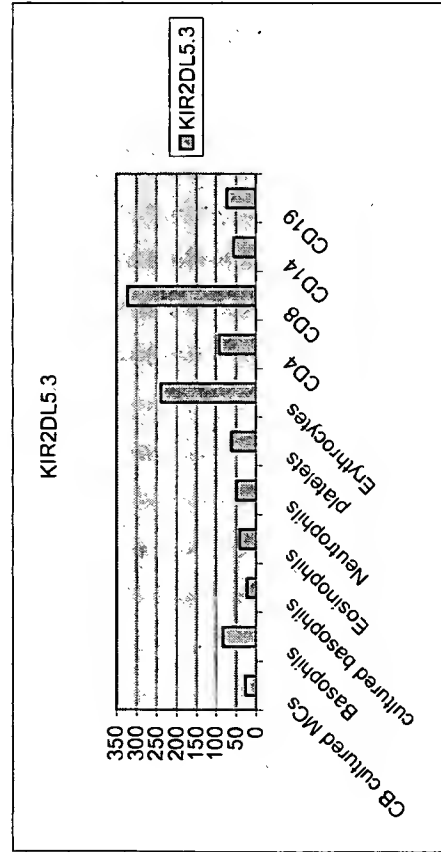
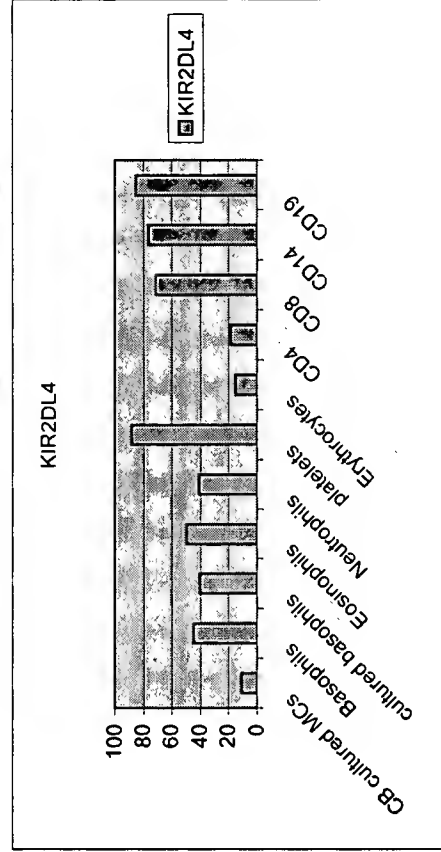
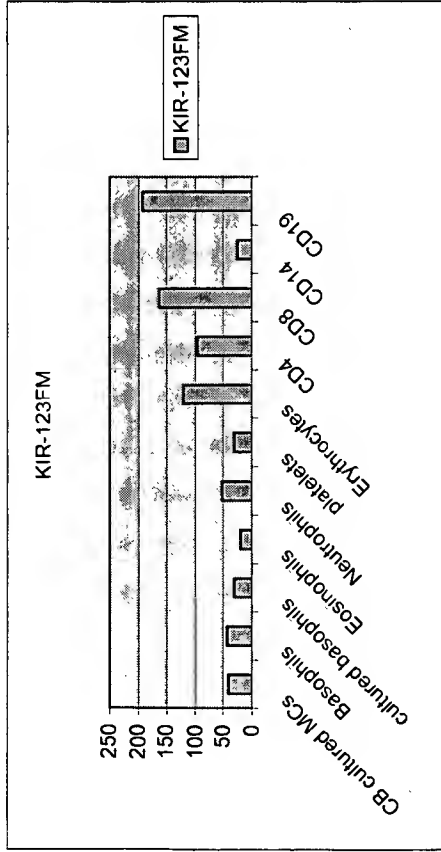


Figure 5D



**Table E1. The complete list of granulocyte subtype-selective transcripts.** Selectivity index (S.I.) was calculated by comparing the "normalized AD" level of a cell type or of two cell types with the maximal gene expression level of the other 8 or 9 cell types including platelets (Pl), CD4<sup>+</sup> cells, CD8<sup>+</sup> cells, CD14<sup>+</sup> cells, CD19<sup>+</sup> cells and nasal polyp-derived cultured fibroblasts (Fb). When the result was accompanied by presence call, it was shown as a bold numeral. Italic numerals show that the raw AD levels were associated with absence call by the GeneChip analysis software. Transcripts having S.I. >3-fold were shown in A-H. Abbreviations used in the table through A-I were (small); the results obtained by the small sample protocol (see materials and methods), R; receptor, and ICN; ion channel.

**A. Basophil (Ba)-selective transcripts (1/2).**

Probe set	Accession #	Transcripts	MC, cord blood	MC, lung	Ba.1 (small)	Ba.2 (small)	Ba.3 (small)	EO 1	EO 2	EO 3 (small)	EO 4 (small)	Ne 1	Ne 2	Ne 3 (small)	Ne 4 (small)	pl	CD4	CD8	CD14	CD19	Fb	Ba.S.I.
207539_s_at	NM_000589.1	IL-4	0.2	0.1	10.4	16.9	13.4	0.1	0.0	0.2	0.1	0.1	0.3	0.0	1.2	0.2	0.0	0.2	0.1	0.0	0.0	73.348
210254_at	L35948.1	HLI-m4	0.8	0.4	115.6	130.1	153.6	2.4	1.7	21.8	1.7	0.1	0.9	3.6	9.5	0.2	0.5	0.4	0.1	0.2	0.0	38.24
205513_at	NM_001062.1	vitamin B12 binding protein	1.5	1.2	98.9	149.3	110.9	3.2	2.2	16.1	1.9	4.9	4.5	6.3	8.1	1.8	0.7	0.8	1.4	0.9	0.1	20.322
206148_at	NM_002183.1	IL-3 R	1.0	0.1	6.2	80.2	71.3	1.7	1.7	1.8	2.9	0.3	0.4	0.2	1.9	0.2	0.3	0.2	0.7	0.1	0.1	16.82
214920_at	R33964	FLJ11022 lis	0.1	1.1	4.9	13.1	15.4	0.1	0.2	0.7	0.5	1.0	0.4	0.5	0.7	0.1	0.1	0.2	0.1	0.3	0.1	16.049
201825_s_at	AL572542	CGI-49	3.3	1.6	21.4	74.9	46.5	2.1	1.2	0.1	1.2	0.1	0.1	0.2	0.1	1.3	0.7	1.7	1.4	0.8	2.8	15.045
213238_at	AI478147	ATPase, Class V, type 10D	1.2	2.9	39.9	76.3	118.9	2.3	1.7	3.1	1.9	2.1	1.4	2.3	8.8	0.7	0.9	0.9	2.5	5.0	4.1	14.398
211734_s_at	BC005912.1	Fc epsilon R1 alpha	10.5	28.4	210.0	220.8	226.2	8.4	2.1	4.8	2.9	0.3	0.7	4.5	18.6	1.4	5.1	0.8	1.4	0.4	0.2	12.703
213894_at	BF447246	KIAA0960	0.1	0.0	3.7	13.0	15.6	0.3	0.4	0.4	0.4	0.9	0.7	0.7	0.6	0.5	0.6	0.1	0.1	0.2	0.2	12.272
206363_at	NM_005360.2	c-MAF	3.7	1.4	36.5	75.7	66.4	1.2	0.1	0.2	0.2	0.2	0.1	0.2	1.0	0.6	4.8	2.7	0.5	1.0	0.0	11.927
203373_at	NM_003877.1	SOC52	2.1	3.9	21.7	85.0	112.2	4.6	4.7	9.4	6.5	0.7	1.2	0.3	2.5	1.6	3.2	3.5	0.8	0.9	3.6	9.8282
213694_s_at	NM_000589.1	IL-4	0.3	0.1	5.4	9.8	9.2	0.4	0.4	0.0	0.3	0.1	0.0	0.4	0.7	0.8	0.4	0.3	0.1	0.0	0.1	9.8156
209360_s_at	BF671400	LIM-protein	0.6	0.1	11.1	21.0	20.6	1.9	1.6	2.4	1.8	0.8	0.6	1.5	2.5	0.1	0.0	0.3	1.0	0.0	0.1	8.9245
202034_at	NM_004056.2	carbonic anhydrase VIII	10.4	2.4	53.2	131.1	90.5	8.5	7.0	13.8	11.3	0.5	0.5	0.5	4.2	1.3	4.1	5.9	1.3	2.5	3.1	8.7543
210843_at	AF053712.1	osteopontin ligand	0.4	0.1	11.7	10.2	8.0	1.2	0.1	0.2	0.4	0.4	0.1	0.3	0.1	0.5	0.5	1.1	0.1	0.1	0.8	8.1309
209211_at	AF132818.1	colon Kruppel-like factor	0.1	0.3	1.8	3.4	6.0	0.7	0.4	0.3	0.2	0.4	0.1	0.3	0.1	0.1	0.3	0.4	0.3	0.2	0.1	7.239
204309_at	NM_000781.1	CYP11A	0.3	0.1	2.6	6.1	5.6	0.1	0.3	0.5	0.5	1.0	0.1	0.1	0.9	0.3	0.3	0.1	0.0	0.3	0.7	6.8366
203372_s_at	AB004903.1	SOC52	0.6	1.6	9.2	8.5	15.9	1.4	2.4	0.9	0.2	0.7	0.6	0.4	0.8	0.8	1.6	1.3	0.3	0.3	1.4	6.8271
207463_x_at	NM_002771.1	serine protease 3 (trypsin 3) acid sphingomyelinase-like phospholipase	1.0	1.0	4.8	10.0	10.9	4.4	1.0	1.0	1.2	1.2	0.9	1.0	1.8	0.4	0.6	0.4	0.3	0.7	1.2	8.7218
213624_at	AA673600	done DKE Zm3400213	4.7	2.0	20.8	30.6	25.9	2.1	2.8	3.8	1.7	0.5	1.1	1.3	1.3	0.1	0.2	0.1	3.8	0.2	3.2	6.8846
214873_at	AL137651.1	protein P3	0.1	0.4	3.7	15.5	24.4	2.0	0.9	2.5	2.3	0.2	0.1	0.7	0.6	0.1	1.1	1.5	0.5	0.6	0.7	6.2585
204928_s_at	NM_019848.2	prostate carcinoma tumor antigen (pca-1)	2.3	1.5	9.8	49.0	34.3	3.7	3.3	4.8	4.2	1.6	1.0	1.9	2.2	4.1	1.8	3.0	0.8	2.0	2.6	6.2142
208035_s_at	L78132.1	phosphatase 2 (PMM2)	2.2	1.2	9.9	19.1	16.6	2.3	1.5	3.6	2.5	1.1	1.1	1.9	0.9	1.8	1.8	2.0	2.0	1.4	0.8	6.2011
203201_at	NM_000303.1	CGI-49	1.8	0.3	10.7	15.9	6.5	0.9	0.6	1.2	0.9	0.8	0.4	1.1	1.3	1.0	1.3	1.2	1.2	1.1	1.7	6.1557
201826_s_at	NM_016002.1	serine protease 4 (trypsin 4)	1.8	3.1	11.0	27.5	15.1	1.6	1.1	1.4	2.1	1.1	1.4	1.3	1.8	1.6	1.1	1.1	1.1	0.6	2.9	5.6407
213421_x_at	AW007273	c-MAF, short form	1.8	1.7	5.9	12.5	11.4	1.0	0.5	1.2	0.5	1.2	1.7	1.2	1.2	0.9	1.0	1.2	1.0	0.4	1.7	5.4802
205348_s_at	AF055376.1	hypothetical protein PP1665	6.4	4.9	29.6	47.7	42.3	0.8	0.3	0.4	0.6	0.3	0.0	0.9	1.4	1.0	7.3	3.1	0.9	0.7	1.4	5.3183
213343_s_at	AL041124	hypothetical protein PP1665	0.9	0.2	12.2	17.0	12.0	3.5	1.7	0.5	0.6	0.1	0.3	0.8	0.4	0.6	1.5	2.6	0.7	1.6	1.3	5.2721
202491_s_at	NM_003640.1	I kappa B-associated protein	1.6	3.8	23.9	51.9	43.5	4.6	4.0	7.1	7.3	1.6	2.1	2.5	2.3	1.7	3.7	7.4	3.2	4.7	4.2	5.107
221021_s_at	NM_030877.1	Bos taurus P14 protein	6.9	3.2	7.2	29.2	58.9	2.8	3.2	5.4	6.3	0.9	1.2	1.8	1.6	1.6	2.2	2.4	2.0	3.5	1.8	4.9129
213346_at	BE748563	hypothetical protein BC015148	2.7	1.8	17.5	38.8	25.8	4.0	6.7	6.2	4.8	1.4	0.9	0.8	1.1	0.2	1.2	1.5	0.6	1.1	1.9	4.8879
209764_at	AL022312	mannosyl (beta-1,4)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase	0.0	0.9	4.1	6.1	5.8	0.8	1.4	0.9	1.4	0.6	0.1	0.5	0.2	1.0	0.4	0.2	0.2	0.4	0.3	4.855
207067_s_at	NM_002112.1	histidine decarboxylase	64.1	14.7	105.2	164.9	165.7	3.4	1.4	4.1	2.8	2.1	1.2	4.6	14.0	2.4	0.8	0.9	1.1	0.7	0.2	4.8305
210375_at	X83858.1	prostaglandin E receptor, type 3a2	1.0	0.6	2.4	11.5	17.0	0.3	0.1	0.1	0.0	0.4	0.7	0.9	0.7	0.6	0.3	0.2	0.2	0.5	1.7	4.6103
206306_at	NM_001036.1	ryanodine receptor 3 (RYR3)	2.1	1.1	3.7	11.0	7.8	1.0	0.6	1.5	0.5	1.2	0.3	1.5	0.9	1.1	0.7	0.3	1.0	0.2	0.4	4.5552
210001_s_at	AB005043.1	SOC51 serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 2 (SERPINB2)	5.2	0.2	3.0	24.1	29.9	2.1	3.0	3.2	3.4	0.3	1.0	0.8	1.3	0.8	0.8	0.8	0.0	0.8	0.9	4.5248
204614_at	NM_002575.1	hepatocyte growth factor (HGF)	0.3	0.6	5.3	12.9	12.5	0.4	2.4	4.2	2.0	1.0	0.8	0.7	0.3	1.9	0.5	0.7	2.1	0.2	0.2	4.5061
209960_at	X16323.1	transcription factor BTEB2	0.4	0.0	2.3	7.3	5.5	0.5	0.4	0.6	0.5	0.1	0.1	1.0	0.6	0.7	0.1	0.0	1.0	0.0	0.5	4.4335
209212_s_at	AB030824.1		0.1	0.2	7.5	14.3	22.1	2.3	2.0	4.9	3.7	1.2	1.3	1.5	2.5	1.4	0.5	0.2	1.1	0.9	0.8	4.363

## A. Basophil (Ba)-selective transcripts (2/2).

Probe set	Accession #	Transcripts	MC, cond blood	MC, lung	Ba 1	Ba 2	Ba 3	Eo 1	Eo 2	Eo 3	Eo 4	Ne 1	Ne 2	Ne 3	Ne 4	pl	CD4	CD8	CD14	CD19	Fb	Ba S.I.
214651_s_at	U41813.1	class I homeoprotein (HOXA9)	-0.5	0.6	1.7	6.3	8.3	0.3	0.5	0.8	0.5	0.1	0.1	0.1	0.5	1.0	1.0	0.1	0.1	0.1	0.1	4.3618
32502_at	AL041124	DKFZp434D0316_s1	1.5	1.9	14.6	22.5	17.4	4.0	2.1	0.7	1.4	1.1	1.0	0.4	0.4	2.3	2.5	4.1	2.5	2.3	1.8	4.3594
205373_at	NM_004389.1	calenin (cadherin-associated protein), alpha 2	0.2	0.1	1.1	3.9	3.2	0.6	0.1	0.1	0.1	0.1	0.1	0.2	0.1	0.1	0.1	0.1	0.6	0.2	0.2	4.2308
219676_at	NM_025231.1	FLJ22191	0.3	0.7	2.5	7.3	12.0	0.9	0.2	2.0	1.5	0.2	1.1	4.2	2.2	0.6	1.1	1.4	0.3	1.4	0.1	4.2135
213385_at	NM_028415.1	beta2-chimaerin	4.7	3.1	8.3	22.9	21.8	1.1	0.8	0.9	1.0	0.2	1.5	0.8	1.0	0.1	0.9	1.6	3.3	0.2	0.4	4.2131
214637_at	BG437034	oncostatin M	0.4	0.0	0.9	5.4	4.4	0.2	0.7	0.1	0.7	0.5	1.8	0.2	1.1	0.4	0.1	0.1	0.2	0.1	0.0	4.1983
202490_at	AF153419.2	Ikappa B-associated protein	0.2	0.2	1.3	3.6	2.2	0.4	0.4	0.5	0.1	0.3	0.0	0.2	0.0	0.3	0.3	0.5	0.2	0.4	0.2	4.1747
220416_at	NM_024837.1	FLJ141472	4.1	1.5	9.1	9.7	12.2	1.9	3.3	3.0	1.9	0.8	0.6	1.1	0.9	0.7	0.6	0.2	0.8	0.3	0.0	4.1718
218318_s_at	NM_016231.1	nemo-like kinase	1.4	1.3	6.2	7.0	7.1	0.8	0.9	0.8	0.6	0.5	1.0	0.1	0.1	1.6	1.3	0.9	1.2	1.1	0.4	4.1558
215201_at	NM_016231.1	FLJ14135 fs, clone MAMMA1002728	0.1	0.1	2.1	3.5	5.1	0.5	0.7	0.8	0.9	0.0	0.1	0.1	0.1	0.1	0.5	0.3	0.8	0.4	0.5	4.1491
222303_at	AW166925	ETS2 intronic transcript 1 mRNA	0.6	1.4	31.1	86.8	63.8	3.6	2.2	2.9	3.2	10.8	10.5	16.6	19.0	1.2	0.7	0.7	8.1	0.3	0.8	4.0555
210694_at	AV700891	DKFZp434F205	2.8	5.0	17.3	27.7	31.8	4.4	5.3	9.1	8.3	4.3	3.9	5.7	5.5	0.1	4.8	4.2	2.5	4.1	4.8	3.8471
210252_s_at	AB002356.1	MAP-kinase activating death domain	5.6	4.6	12.7	35.0	40.7	6.2	6.1	7.0	8.3	2.2	1.3	1.9	3.3	5.2	2.7	5.4	3.0	3.5	1.1	3.8424
201328_at	AL575509	vets avian erythroblastosis virus E26 oncogene homolog 2	1.7	0.1	18.4	34.7	50.7	2.8	1.6	1.7	1.8	6.4	9.9	8.7	8.9	0.5	0.9	1.0	4.4	0.1	1.7	3.8075
218392_x_at	NM_022754.1	FLJ12876	1.2	1.0	3.5	7.5	7.4	1.4	1.0	2.7	1.5	1.0	0.6	0.9	0.1	0.9	1.4	0.4	0.7	0.5	1.4	3.7693
205046_at	NM_001813.1	FLJ14150 fs, clone MAMMA1003026	0.0	0.3	1.5	8.1	13.1	1.7	0.5	1.9	1.2	0.5	1.3	1.0	0.9	1.1	1.5	0.9	1.0	0.4	0.2	3.7324
221170_at	AF312230.1	histamine H4 receptor	0.6	0.8	35.9	34.2	32.5	7.8	11.9	8.7	9.3	0.2	0.8	0.8	1.0	0.4	0.8	0.5	0.6	0.0	0.1	3.6719
201663_s_at	NM_005406.1	chromosome-associated polypeptide C	2.2	4.3	17.6	15.1	18.1	3.4	8.8	4.9	4.2	4.0	3.7	2.2	2.7	1.7	4.1	2.9	1.7	3.7	4.2	3.6472
208933_s_at	AL659005	lectin, galactoside-binding, soluble, 8	11.8	4.9	28.7	28.3	28.2	5.9	6.8	10.1	4.8	3.8	4.5	5.5	2.1	4.3	7.6	7.4	7.2	4.3	2.7	3.6311
209710_at	AL563460	GATA-binding protein 2	50.4	38.9	141.1	189.2	154.7	4.4	1.3	3.8	3.1	0.7	1.2	5.4	10.8	2.5	0.7	0.9	0.3	0.1	6.3	3.6251
205769_at	NM_003645.1	fatty-acid-Coenzyme A ligase, very long-chain 1 (FACVL1)	3.3	2.5	7.0	16.2	9.2	0.3	0.3	0.3	0.5	0.1	0.4	0.2	0.3	0.2	0.4	0.7	0.1	0.3	0.1	3.5389
209409_at	D86982.1	KIAA0207	8.4	2.6	12.5	38.0	33.1	4.9	4.2	12.3	10.4	1.7	1.7	2.1	1.8	1.4	0.4	0.7	1.5	0.4	4.8	3.4907
38398_at	AB002336	KIAA0388	5.5	4.1	13.8	24.6	29.8	6.1	6.4	5.6	7.0	3.0	3.2	3.3	4.1	5.1	3.3	5.3	3.7	4.4	2.5	3.4534
205899_at	NM_003914.1	cyclin A1	5.6	3.6	16.2	20.6	10.5	0.1	0.6	0.9	0.1	1.6	0.1	0.8	0.4	1.9	0.7	0.1	0.1	0.3	0.8	3.3824
218150_at	NM_012097.1	ADP-ribosylation factor-like 5	8.2	5.3	37.6	56.6	54.6	9.1	8.6	14.0	12.1	3.9	5.0	7.7	9.6	3.8	8.3	8.1	14.5	9.9	8.1	3.3745
213097_s_at	A1338837	zardin related factor 1	2.1	1.8	8.4	13.4	16.7	4.8	2.1	4.8	3.7	1.8	1.2	1.2	1.6	0.3	3.4	3.7	2.3	3.3	2.8	3.3672
208158_s_at	NM_018030.1	oxysterol-binding protein-related protein	1.2	2.3	8.8	18.0	15.3	0.6	0.8	1.6	1.4	1.5	2.3	2.7	1.8	2.0	0.2	0.7	1.3	0.5	4.0	3.342
210109_at	AF191492.1	nasopharyngeal carcinoma associated gene protein-8	1.2	0.7	3.6	6.4	4.2	1.2	1.6	1.0	0.3	0.6	1.1	1.7	0.6	0.2	1.3	0.5	1.4	0.6	0.1	3.2977
220918_at	NM_025143.1	eml 1 (acute myeloid leukemia 1)	1.0	1.1	26.1	37.3	26.2	6.2	6.5	14.1	11.3	3.3	2.5	2.0	2.0	1.1	0.9	0.9	3.5	1.1	0.1	3.2902
209359_x_at	L34598.1	oncogene	1.2	0.1	3.1	7.2	7.1	2.5	1.6	1.6	1.1	0.2	1.0	0.6	1.4	0.7	0.7	1.0	0.8	0.6	0.1	3.2789
208107_s_at	NM_030941.1	exonuclease NEF-sp	3.6	7.6	7.8	30.6	20.1	1.6	2.3	2.7	0.8	0.6	0.2	1.5	1.0	0.2	0.1	0.3	0.2	0.1	1.2	3.2356
212412_at	AV715767	DKFZp664A072	18.2	16.2	41.3	72.5	67.3	7.7	7.7	16.3	11.6	6.4	6.3	9.1	12.7	3.7	3.1	4.1	8.0	3.3	18.3	3.2017
215215_s_at	AC004381	chromosome 16 BAC clone	2.9	2.5	4.8	12.8	10.4	0.6	0.9	1.4	0.8	0.1	0.0	0.2	0.8	0.1	0.4	0.3	0.4	0.3	0.5	3.198
221509_at	AB014731.1	SMAP-3	7.6	5.4	13.2	48.5	32.4	5.2	5.7	18.1	10.7	3.5	3.8	11.4	8.1	2.8	5.8	6.0	4.1	7.5	8.0	3.1618
218637_at	NM_018439.1	hypothetical protein IMPACT	1.3	2.4	2.9	10.7	9.3	1.5	1.5	2.7	2.1	0.6	0.7	0.6	0.6	1.2	0.8	0.7	0.9	1.1	2.1	3.1587
218352_at	NM_018191.1	hypothetical protein FLJ10716	0.8	0.5	4.9	13.7	8.7	2.3	1.7	3.4	3.9	1.0	2.0	2.8	3.6	0.8	2.3	2.0	1.7	2.2	2.4	3.1058
213035_at	A081194	KIAA0379	2.1	3.8	11.1	26.7	22.4	2.5	1.5	3.4	2.5	1.9	1.1	2.3	1.6	4.6	2.5	1.3	0.1	2.2	8.1	3.0937
211180_x_at	D89788.1	ami 1 (acute myeloid leukemia 1) oncogene	1.5	0.2	3.1	9.4	7.5	2.0	2.5	1.7	1.7	1.0	1.4	0.3	1.1	0.4	0.4	0.6	1.1	0.7	0.2	3.0936
210731_s_at	AL136105	lectin, galactoside-binding, soluble, 8	2.1	1.1	4.8	9.1	6.4	1.9	1.8	3.0	1.8	1.2	1.4	2.7	1.6	2.1	1.2	1.2	1.7	1.3	0.9	3.0876
203164_at	BE464756	acyl-Coenzyme A transporter	2.3	1.9	3.7	12.6	12.4	2.5	1.9	4.0	2.7	1.1	0.6	1.2	1.7	1.4	2.3	2.6	2.1	2.7	2.5	3.063
205768_s_at	NM_003645.1	fatty-acid-Coenzyme A ligase, very long-chain 1 (FACVL1)	3.0	1.7	3.9	10.7	7.7	0.4	0.1	0.6	0.2	0.1	0.8	0.1	0.7	0.0	0.8	0.1	0.2	0.1	0.1	3.0353
210517_s_at	AB003476.1	A kinase (PRKA) anchor protein (gravin) 12	25.1	4.9	44.0	69.5	59.6	1.5	0.4	0.6	0.8	0.1	0.2	1.0	3.0	0.9	0.8	0.5	0.1	0.3	18.8	3.0146
210647_x_at	AF102988.1	Ca2+-independent phospholipase A2 short isoform	2.3	1.1	18.7	13.2	9.1	3.4	3.3	4.0	4.5	3.3	5.0	4.2	3.6	1.8	3.5	4.4	1.8	2.8	2.2	3.002

## B. Eosinophil (Eo)-selective transcripts (1/1).

Probe set	Accession #	Transcripts	MC, cord blood	MC, lung	Ba	Ba 2 (small)	Ba 3 (small)	Eo 1	Eo 2	Eo 3 (small)	Eo 4 (small)	Ne 1	Ne 2	Ne 3 (small)	Ne 4 (small)	pl	CD4	CD8	CD14	CD19	Fb	Es S.I.
207328_at	NM_001140.1	15-lipoxygenase	0.1	0.6	0.7	0.1	0.1	14.5	24.6	18.3	17.0	0.1	1.1	0.1	0.1	0.1	0.0	0.1	0.0	0.1	0.0	74.129
219695_at	NM_024703.1	FLJ22593	0.0	1.0	1.8	1.8	1.1	29.8	34.7	24.8	27.8	0.8	1.5	0.4	0.9	0.1	0.6	0.4	0.3	0.1	0.1	19.123
208253_at	NM_014442.1	sialic acid binding Ig-like lectin, Siglec 8	1.3	2.4	0.4	0.4	0.2	17.1	23.1	17.6	11.8	0.1	0.4	0.1	0.8	0.3	0.2	0.1	0.2	0.5	0.2	9.8056
211922_s_at	AY028632.1	catalase	3.7	2.2	6.2	6.8	2.2	78.2	134.5	119.7	88.8	16.2	13.0	8.8	8.7	0.7	2.2	2.9	11.1	7.5	4.6	9.125
201802_at	NM_004955.1	solute carrier family 29 (nucleoside transporters)	4.8	2.8	2.9	3.4	1.9	24.8	30.4	36.1	42.3	0.1	0.6	0.6	0.8	0.2	0.9	0.3	2.2	1.0	1.1	8.989
214523_at	NM_001805.1	CCAAT enhancer binding protein (CEBP), epsilon	0.1	0.1	0.7	1.2	1.2	7.9	11.4	23.4	17.3	1.8	1.5	1.9	1.1	1.4	0.5	0.4	1.0	0.1	0.1	8.9462
210029_at	M34455.1	interferon-gamma-inducible indoleamine 2,3-dioxygenase	0.7	0.1	5.3	4.2	2.6	20.0	39.0	33.4	29.5	1.6	2.1	2.3	1.8	1.7	1.5	1.7	0.3	1.4	0.9	7.7078
215573_at	AU147084	FLJ12072	0.1	0.1	0.5	0.3	1.1	9.8	8.4	16.9	7.2	0.4	1.9	1.8	2.0	0.1	0.1	0.0	0.1	0.4	0.0	7.5983
201801_s_at	AF079117.1	solute carrier family 29 (nucleoside transporters)	3.5	1.9	1.7	0.5	0.9	29.7	47.1	7.4	11.0	0.1	0.5	0.4	0.7	1.1	0.4	0.1	1.4	0.6	1.0	7.0314
213825_at	AF221520.1	oligodendrocyte lineage transcription factor 2	0.4	0.6	0.2	0.4	0.6	6.0	10.9	18.7	12.5	0.8	0.9	1.5	1.0	0.6	1.7	0.3	0.4	0.3	0.3	6.5987
219821_s_at	NM_018988.1	glucose-fructose oxidoreductase domain containing	3.0	1.4	1.8	2.6	2.3	18.7	17.3	30.9	31.3	3.9	3.1	2.4	2.9	3.2	1.3	2.5	3.0	3.8	0.8	6.2284
205472_s_at	NM_004392.1	dachshund (Drosophila) homolog	0.0	0.1	0.1	0.4	0.1	2.7	1.4	2.2	1.7	0.3	0.1	0.1	0.1	0.2	0.1	0.1	0.1	0.3	0.0	6.0088
202188_at	NM_014669.1	KIAA0095	0.5	0.9	0.4	1.8	1.2	6.8	8.5	13.5	10.6	0.2	0.2	0.2	0.1	0.2	0.3	1.7	1.7	1.4	0.4	5.4499
210548_at	U58913.1	chemokine CCL23	0.6	1.8	0.4	1.1	0.5	5.5	6.2	4.2	6.9	0.1	0.9	0.1	0.2	0.3	0.1	0.2	0.6	0.1	0.0	5.3082
209447_at	AF043290.1	lymphocyte membrane associated protein (BB7)	0.6	0.5	2.5	3.4	3.6	41.8	49.7	56.2	60.1	0.2	0.9	0.5	1.2	2.6	5.1	10.4	1.6	8.3	2.7	5.1472
206171_at	NM_000677.2	ADORA3 adenosine A3 receptor	2.3	2.8	2.8	3.7	2.2	7.8	13.9	22.0	17.9	1.6	3.1	2.2	2.5	1.2	1.6	0.5	2.0	0.5	0.5	5.0469
210549_s_at	U58913.1	chemokine CCL23	1.1	1.1	0.1	1.3	0.6	7.9	5.6	2.7	8.1	0.0	0.6	0.0	0.2	0.1	0.1	0.1	0.2	0.0	0.4	4.9873
214183_s_at	X91817.1	transketolase-like protein spectrin repeat containing, nuclear envelope 1	0.1	0.2	0.2	0.1	0.1	3.2	4.0	8.8	7.2	0.2	0.2	0.1	0.1	0.2	0.2	1.0	0.1	0.6	0.0	4.7894
215350_at	AB033088.1	P2Y2 purinergic receptor	0.1	0.1	0.5	0.1	0.1	3.8	4.2	3.0	2.8	0.0	0.1	0.2	0.4	0.7	0.2	0.1	0.0	0.1	0.2	4.7822
206277_at	NM_002564.1	thrombospondin 4 (THBS4)	0.1	0.1	0.1	0.2	0.1	3.4	4.7	8.1	5.9	0.1	0.3	0.1	0.1	0.2	0.1	0.3	1.2	0.2	0.1	4.3043
204776_at	NM_003248.1	L-iditol-2 dehydrogenase	0.8	0.1	1.5	0.1	0.8	3.2	5.9	10.0	6.4	1.8	1.4	0.6	0.9	0.3	0.2	0.3	1.4	1.1	1.2	4.1746
201563_at	L29008.1	P2YX purinergic receptor GPR105 for UDP-glucose	4.1	2.6	3.5	11.4	12.8	22.5	29.9	49.0	37.0	1.8	3.0	4.4	2.2	2.1	1.5	1.2	2.7	2.5	1.8	4.1557
206637_at	NM_014879.1	collagen, type IX, alpha 2	5.7	1.6	13.3	19.9	13.5	44.2	55.1	81.4	62.4	1.8	9.3	15.4	9.2	0.7	0.9	0.8	0.0	5.5	0.1	3.8761
213622_at	A1733465	PDZ domain protein	1.5	1.4	1.9	1.2	1.3	10.3	9.6	6.6	8.8	2.7	2.1	2.1	2.2	0.7	1.2	1.2	2.2	1.7	0.9	3.8576
214705_at	AJ001306.1	CD24 signal transducer	0.1	0.1	0.4	0.3	0.1	2.1	1.5	2.6	2.2	0.3	0.0	0.6	0.7	0.1	0.4	0.3	0.3	0.6	0.1	3.6532
266_s_at	L33930	catalase (CAT)	0.2	0.1	3.0	0.3	0.8	11.9	14.0	18.8	13.9	0.1	0.1	0.3	0.8	0.9	0.0	0.1	0.1	4.3	0.2	3.3793
201432_at	NM_001752.1	fructose-1,6-bisphosphatase	23.0	14.3	35.7	49.4	19.9	202.3	209.7	221.8	207.3	67.0	54.3	71.3	60.9	9.2	11.2	15.1	53.6	29.9	21.4	3.3325
208696_at	D26054.1	CD24 signal transducer	0.9	3.4	4.3	11.1	6.4	20.2	27.7	28.8	32.5	3.0	2.5	2.4	1.6	1.9	2.0	1.6	8.1	1.1	0.6	3.3089
216379_x_at	AK000168.1	lysosome-associated membrane glycoprotein (LAMP1)	1.3	1.4	16.2	0.9	1.5	66.1	70.1	81.9	77.9	1.7	2.8	2.6	4.1	4.8	0.5	0.6	0.9	22.5	0.5	3.2741
205569_at	NM_014398.1	hypothetical protein PRQ2521	0.4	0.2	0.7	0.1	0.4	2.4	3.1	6.8	3.0	0.6	0.1	1.4	0.8	0.4	1.1	0.7	0.1	0.0	0.3	3.2308
219233_s_at	NM_018530.1	gastrointestinal tumor-associated antigen GAT33.1	0.1	1.9	2.1	4.6	5.4	7.5	8.5	21.8	21.2	0.8	0.1	1.5	2.1	0.1	1.1	4.1	0.1	1.4	0.5	3.2093
202286_s_at	J04152	Bloom syndrome	0.9	0.7	1.3	0.3	0.1	1.1	2.5	8.7	1.8	0.4	0.8	0.6	0.6	0.2	0.2	0.7	0.3	0.5	0.1	3.1844
206442_at	NM_003007.1	calicium/calmodulin-dependent protein kinase 1 (CAMK1)	0.6	0.1	0.4	0.0	0.1	1.2	3.2	4.9	3.4	0.3	0.2	1.1	1.9	0.1	0.2	0.2	0.9	0.4	0.1	3.1837
205733_at	NM_000057.1	DKFZp586C1619	1.9	1.1	2.0	2.4	2.2	8.5	6.0	7.5	11.2	2.1	2.0	1.0	1.2	1.2	2.4	1.8	1.1	2.6	1.2	3.1427
204392_at	NM_003656.2	similar to ankyrin repeat-containing protein AKR1	4.0	1.1	6.3	8.9	6.4	17.8	19.3	24.9	26.5	0.6	0.2	1.8	1.5	0.1	1.4	1.0	3.0	0.6	1.8	3.0763
213497_at	AL050374.1		1.0	0.7	1.0	1.3	1.6	8.3	6.8	6.8	6.0	2.3	3.0	1.4	2.3	2.0	0.4	0.5	1.6	1.1	0.8	3.0099
219206_at	NM_019028.1		2.2	1.7	0.2	3.5	1.6	7.3	4.4	8.4	7.4	1.8	2.4	2.4	2.3	0.1	1.4	1.6	1.3	1.9	0.8	3.0018

## C. Neutrophil (Ne)-selective transcripts (1/7).

Probe set	Accession #	Transcripts	MC. cord blood	MC. lung	Ba 1	Ba 2 (small)	Ba 3 (small)	Eo 1	Eo 2	Eo 3 (small)	Eo 4 (small)	Ne 1	Ne 2	Ne 3 (small)	Ne 4 (small)	pl	CD4	CD8	CD14	CD19	Fb	Ne.SL
205403_at	NM_004633.1	R interleukin 1 R, type II	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	37.4	41.4	73.8	61.5	0.2	0.4	0.1	0.2	0.0	0.0	127.86
216782_at	AK026679.1	FLJ23026 fs KCNJ15 inward rectifier potassium channel Kir1.3	0.0	0.2	-0.2	0.1	0.1	0.1	0.1	0.5	0.2	33.2	31.5	33.0	17.4	0.1	0.1	0.1	0.1	0.2	0.2	112.28
210119_at	U73191.1	ICN chitinase 3-like 1 (cartilage glycoprotein-39)	0.7	1.1	0.1	0.1	0.5	0.1	0.1	0.9	0.6	81.6	98.6	129.0	88.8	0.7	0.2	0.0	0.8	0.0	0.0	107.47
206395_at	M80927.1	protease inhibitor 3, skin-derived (SKALP)	1.5	0.2	0.9	0.1	0.4	0.3	0.1	8.1	0.1	28.9	25.3	70.7	40.7	0.1	0.0	0.1	0.1	0.1	0.0	79.595
203691_at	NM_002638.1		0.2	0.1	0.1	0.1	0.8	0.5	0.2	0.4	0.1	16.9	36.7	27.7	24.5	0.1	0.1	0.1	0.1	0.5	0.1	51.901
211372_s_at	U64094.1	R interleukin 1 R, type II	0.1	0.2	0.1	0.1	0.0	0.1	0.5	0.7	0.1	21.6	36.5	31.4	29.9	0.3	0.2	0.0	0.6	0.0	0.0	50.606
207008_at	NM_001557.1	GPR CXCR2 interleukin 8 receptor, beta	0.0	0.4	1.1	1.2	1.0	1.3	1.3	2.1	1.2	129.8	188.4	81.5	68.8	2.7	0.3	0.8	0.7	0.6	0.0	39.316
206515_at	NM_000896.1	leukotriene B4 omega hydroxylase (CYP4F3)	0.3	0.1	1.1	0.7	1.2	0.5	0.8	5.9	1.7	56.8	40.3	57.2	48.9	0.2	0.9	0.0	0.7	0.3	0.3	34.919
204007_at	J04162.1	R Fc gamma R IIb (CD16)	0.8	0.7	1.4	1.6	1.8	1.1	1.8	2.8	1.9	204.5	226.5	194.0	173.3	6.6	1.3	1.3	2.2	2.6	0.1	29.895
204470_at	NM_001511.1	melanoma growth stimulating activity, alpha	1.2	0.0	0.7	0.9	0.1	0.6	0.5	1.2	0.7	19.1	23.0	26.3	48.1	0.1	0.2	0.2	1.0	0.1	0.2	28.189
206025_s_at	AW188198	tumor necrosis factor, alpha-induced protein 6	0.1	0.3	0.1	0.6	0.4	0.6	0.1	0.2	0.1	19.0	29.9	17.2	24.7	0.1	0.2	0.2	0.8	0.3	0.6	26.336
209396_s_at	M80927.1	chitinase 3-like 1 (cartilage glycoprotein-39)	1.8	0.2	1.6	0.4	0.5	0.8	0.5	5.6	0.9	37.9	32.2	52.8	26.7	1.4	0.0	0.0	0.1	0.1	0.4	25.669
211806_s_at	D87291.1	ICN KCNJ15 inward rectifier potassium channel Kir1.3	0.9	1.7	2.0	1.4	1.4	2.1	1.3	1.8	1.7	62.2	77.2	77.5	56.8	3.0	1.0	1.1	1.7	0.9	0.7	22.254
221920_s_at	BE677761	mitochondrial solute carrier CXCR1 interleukin 8 receptor, alpha	0.4	0.8	6.9	0.0	0.2	2.4	1.5	2.2	1.5	59.0	43.2	57.4	48.8	2.5	0.7	0.3	1.8	1.1	1.0	20.163
207094_at	NM_000634.1	GPR 23614 mRNA sequence	0.3	0.1	4.2	4.3	4.4	0.3	0.3	0.2	0.3	69.2	81.9	95.3	87.4	0.4	0.3	0.2	0.2	0.1	0.1	19.325
213589_s_at	AW468201	PAR2 proteinase activated receptor-2	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.2	0.1	5.5	2.7	5.1	4.0	0.1	0.1	0.2	0.1	0.1	0.0	18.973
218963_s_at	NM_015515.1		0.0	0.1	0.5	0.3	0.1	1.1	2.8	2.8	2.0	48.3	32.5	40.3	31.3	0.3	0.3	0.1	0.1	0.1	0.1	18.3
213506_at	BE965369	GPR	0.1	0.0	0.0	0.4	0.3	1.2	1.3	4.1	2.3	33.4	35.7	42.4	33.4	0.1	0.7	0.1	1.8	0.4	1.2	18.208
220187_at	NM_024636.1	FLJ23153 tumor necrosis factor, alpha-induced protein 6	0.3	0.1	0.3	0.1	0.1	0.0	0.1	0.5	0.5	16.5	26.3	5.7	7.0	0.0	0.1	0.1	0.7	0.1	0.2	17.111
206026_s_at	NM_007115.1	elafin	0.1	0.8	0.4	0.8	0.6	1.1	0.5	0.9	0.1	18.2	23.3	20.0	17.0	0.6	1.0	1.0	1.1	0.1	1.0	17.051
41469_at	L10343	ICN aquaporin 9	1.2	0.7	1.2	0.8	0.8	0.9	1.0	0.7	0.8	16.2	39.1	19.5	17.4	1.3	1.4	0.7	0.8	0.5	0.5	15.913
205588_at	NM_020980.2	R decoy receptor 1, TRAILR3	0.5	0.9	0.1	-0.1	0.1	0.3	0.1	1.0	0.1	133.3	136.7	169.0	110.5	0.4	0.9	0.1	8.6	0.1	0.2	15.805
210483_at	BC005043.1	R superoxide dismutase 2	0.1	0.1	0.4	0.9	0.7	1.0	0.9	1.3	1.2	25.8	23.2	9.7	8.6	0.2	0.4	0.3	0.2	0.2	0.1	13.337
215223_s_at	W46388	R	4.4	1.9	1.7	4.9	8.7	5.8	3.3	6.0	8.3	124.6	153.1	142.4	151.8	11.0	1.6	1.1	7.3	2.2	1.5	13.008
210484_s_at	BC005043.1	decoy receptor 1, TRAILR3 complement component 4-binding protein, alpha	0.9	0.9	0.9	0.2	0.1	2.2	4.8	0.8	0.6	60.1	86.3	4.7	5.9	0.5	0.6	0.4	0.9	0.4	0.5	12.748
205654_at	NM_000715.1	GPR formyl peptide receptor 2	0.5	1.1	1.3	0.7	0.7	1.5	1.0	1.3	1.4	2.1	20.7	43.6	33.7	1.2	0.3	1.3	1.2	1.2	0.9	12.161
210773_s_at	U81501.1	R	0.8	0.1	0.6	0.6	0.3	0.6	0.6	0.6	0.5	86.9	105.0	50.2	59.9	0.1	1.0	0.6	6.0	0.8	0.1	12.14
206222_at	NM_003841.1	SEC14 (S. cerevisiae)-like 1	1.5	0.8	1.9	0.7	0.7	3.6	13.7	3.4	3.9	121.0	137.1	37.5	22.5	0.0	0.1	0.1	1.8	0.5	0.7	12.034
207083_s_at	NM_003003.1	R	0.8	0.2	0.9	1.8	3.0	2.2	2.6	3.8	2.6	36.7	25.9	33.9	32.6	1.3	0.1	0.1	1.1	1.0	0.7	11.729
211163_s_at	AF012536.1	decoy receptor 1, TRAILR3 cAMP response element-binding protein CREBPA	0.2	0.1	2.2	1.5	0.6	2.6	12.3	9.4	6.4	87.9	110.9	60.4	55.8	0.5	0.2	0.1	0.7	0.1	0.6	11.404
205931_s_at	NM_004904.1	vanin 2	0.0	0.1	0.3	0.1	0.6	0.6	0.6	0.6	0.7	23.2	14.5	20.5	12.9	1.6	0.8	0.1	1.6	0.1	0.1	10.618
205922_at	NM_004665.1	R Toll-like receptor 1	0.1	0.0	1.2	2.6	3.9	1.0	0.2	1.9	0.3	114.5	114.6	174.1	189.2	0.1	1.4	4.0	13.8	1.7	0.0	40.451
210176_at	AL050262.1	liver-type alkaline phosphatase	0.7	0.6	0.2	0.3	0.3	0.5	1.1	1.9	1.2	29.5	36.6	25.1	32.6	1.6	0.8	0.7	3.0	1.5	0.3	10.418
215977_x_at	X68285.1	GK gene for glycerol kinase, exon 1	1.9	0.9	-0.8	0.7	1.0	0.3	0.6	0.9	1.0	15.8	19.8	9.7	10.9	0.1	0.1	0.2	0.2	0.2	0.3	10.203
215783_s_at	X14174.1		0.5	1.2	0.7	0.9	0.4	0.7	0.5	1.0	0.6	21.2	42.8	11.8	12.8	1.2	0.7	0.2	0.5	0.5	1.9	10.167
217167_x_at	AJ252550		1.2	0.1	0.2	0.3	1.0	0.2	0.1	0.8	0.3	8.0	13.6	7.5	7.2	0.4	0.1	0.1	0.9	0.2	0.2	10.067
213349_at	A934469		0.9	0.7	0.9	1.4	1.0	1.9	1.4	2.3	2.1	15.6	15.3	19.5	23.8	0.1	1.4	1.5	1.6	1.2	1.2	9.7704

## C. Neutrophil (Ne)-selective transcripts (2/7).

Probe set	Accession #	Transcripts	MC, cord blood	MC, lung	Ba 1	Ba 2 (small)	Ba 3 (small)	EO 1	EO 2 (small)	EO 3 (small)	EO 4 (small)	Ne 1	Ne 2	Ne 3 (small)	Ne 4 (small)	pI	CD4	CD8	CD14	CD19	Fb	Ne S.I.
210789_x_at	U00692.1	carcinoembryonic antigen (CGM1)	1.1	0.4	1.9	1.4	1.5	2.0	1.5	2.5	0.4	19.4	18.6	22.6	15.5	0.7	1.6	0.9	2.0	0.3	1.1	9.2749
210772_at	M88107.1	formyl peptide receptor 2	0.1	0.2	0.4	0.7	0.7	0.7	0.3	0.8	0.7	51.4	67.7	44.8	46.4	0.5	0.5	0.5	5.6	0.1	0.1	9.2661
218978_s_at	NM_018586.1	PRO1594	0.7	0.5	1.6	0.2	0.5	1.1	0.9	0.7	0.5	26.3	20.5	8.6	2.8	0.2	0.7	0.4	1.1	0.2	0.4	9.1536
204006_s_at	NM_000570.1	R Fc gamma R IIb (CD16)	0.7	0.2	1.2	0.7	0.6	0.7	0.8	0.0	0.7	230.7	278.8	47.6	45.9	4.2	1.9	6.9	12.0	3.9	0.1	9.0769
207275_s_at	NM_001995.1	fatty-acid-Coenzyme A ligase, long-chain 1 (FACL1)	4.3	2.6	5.1	11.5	19.4	5.3	5.1	5.9	3.7	93.8	127.8	92.8	89.1	0.7	1.0	1.1	8.3	0.9	1.7	8.9855
220302_at	NM_005906.2	nucleic acid-associated kinase	0.1	0.0	1.3	0.7	0.8	0.7	0.2	2.0	1.4	7.9	8.4	7.9	8.9	0.3	0.1	0.0	0.1	0.1	0.0	8.866
221803_s_at	AA883074	KCNJ2 inwardly-rectifying potassium channel Kir2.1	1.1	0.8	3.2	4.0	2.9	2.8	2.8	4.7	3.2	24.7	25.2	33.2	29.3	0.1	1.5	1.2	1.7	2.0	2.6	8.3788
206765_at	AF153820.1	ICN	1.0	0.4	2.5	4.4	4.4	2.4	4.7	6.1	8.0	25.8	36.2	52.4	48.3	0.4	0.2	0.5	1.5	0.7	1.1	8.108
213351_s_at	A034469	KIAA0779	0.0	0.1	0.9	2.0	1.6	0.8	0.6	2.3	2.7	7.9	5.9	20.1	18.0	0.2	0.5	0.2	0.1	0.2	1.2	7.9705
214590_s_at	AL545760	ubiquitin-conjugating enzyme E2D 1 leukotriene B4 omega hydroxylase (CYP4F3)	0.1	1.5	0.3	0.4	0.5	1.1	1.0	0.5	0.4	7.9	10.7	10.1	4.4	0.1	0.4	0.3	1.0	0.4	0.9	7.8712
206522_at	NM_004668.1	R Fc gamma receptor IIC2	0.0	0.0	0.8	1.8	1.0	3.0	5.4	11.7	9.4	46.0	51.5	56.9	43.0	0.1	0.0	0.0	0.6	0.6	0.1	7.5773
210992_x_at	U09039.1	VNNS protein	1.9	1.0	1.7	2.1	3.3	8.1	16.1	2.8	4.2	70.9	95.6	42.8	30.5	0.3	0.2	0.1	7.2	2.3	0.2	7.5239
205298_at	NM_018399.1	early development regulator 2	0.1	0.2	1.3	8.1	5.0	0.2	0.1	0.5	0.4	26.8	22.1	20.0	36.8	0.8	0.2	0.1	3.0	0.1	0.1	7.5216
200919_at	NM_004427.1	glycerol kinase	5.6	4.4	4.8	6.5	9.6	7.6	6.8	5.3	7.3	109.5	89.0	52.9	61.4	2.5	4.9	7.0	10.0	3.9	6.5	7.5056
207397_s_at	NM_000167.1	heat-shock protein HSP70B	2.1	1.5	1.0	1.5	1.6	1.1	1.4	1.6	1.4	14.3	20.3	10.7	10.3	0.9	0.6	0.3	1.7	0.6	0.6	7.4603
117_at	X51757	glutaminyl-peptide cyclotransferase	1.1	0.2	0.8	0.6	0.9	5.9	8.3	2.1	4.1	46.3	41.2	25.1	25.8	0.4	0.9	0.6	3.7	1.6	0.5	7.4139
205174_s_at	NM_012413.2	integrating receptor expressed on myeloid cells 1	0.4	0.0	0.4	0.7	0.9	0.7	0.0	0.4	0.3	30.1	47.7	36.4	24.7	0.7	0.6	0.0	4.6	0.1	1.5	7.3248
219434_at	NM_018643.1	thrombospondin 1	1.3	0.3	0.4	0.2	0.5	2.9	0.7	1.4	1.5	92.8	84.0	81.2	98.8	3.4	0.6	0.1	12.3	0.9	0.3	7.2368
203887_s_at	NM_000361.1	orosomucoid 1 (ORM1)	1.7	0.1	0.4	0.4	0.4	0.2	1.0	1.4	1.1	16.8	13.0	13.4	1.3	0.7	0.6	0.4	1.1	0.4	0.2	7.1328
205040_at	NM_000607.1	glycerol kinase	0.5	0.1	0.1	0.4	0.1	0.1	0.0	1.1	0.0	3.4	4.1	4.3	0.7	0.1	0.3	0.1	0.4	0.0	0.2	7.0823
214681_at	A030490	FLJ20273	0.2	0.4	0.1	1.2	1.7	0.8	1.1	0.6	1.2	7.8	14.2	24.0	12.1	0.9	0.0	0.1	1.9	1.0	0.3	6.966
218035_s_at	NM_019027.1	secretory leukocyte protease inhibitor (antileukoproteinase) (SLPI)	2.9	1.0	0.9	1.5	0.8	0.9	0.4	1.3	1.1	47.2	54.4	91.9	94.0	1.7	0.7	0.4	9.9	1.5	0.3	8.9074
205088_s_at	BE571084	glycerol kinase pseudogene, chromosome 1	1.2	1.4	3.5	5.9	5.1	6.5	5.1	8.5	7.1	43.7	40.6	45.2	56.0	0.7	1.3	2.9	5.1	0.8	1.2	6.8934
203021_at	NM_003064.1	carcinoembryonic antigen subdomains A and B	1.7	0.8	4.6	1.5	1.1	1.2	2.2	8.5	0.8	16.2	19.8	13.9	8.7	1.8	0.6	1.2	1.7	1.1	2.1	6.7497
216316_x_at	X78713	putative lymphocyte GOG1 switch gene (GOS2)	2.0	0.9	0.4	0.6	1.0	0.7	0.6	0.5	1.0	10.3	18.6	5.8	5.8	0.5	0.2	0.2	0.8	0.3	0.1	6.6675
217209_at	X16454	transducin-like enhancer of split 3	0.6	0.4	0.2	0.2	0.4	0.1	0.3	0.7	0.5	2.8	3.8	3.3	2.7	0.3	0.4	0.0	0.1	0.1	0.2	6.5382
220421_at	NM_024850.1	KIAA1547	0.3	0.6	0.1	0.1	0.1	0.3	0.8	0.4	0.3	8.9	7.2	9.1	7.0	1.2	0.6	0.0	0.1	0.1	0.2	6.4857
213524_s_at	NM_015714.1	granulocyte colony-stimulating factor receptor	0.8	0.8	1.3	0.9	0.5	8.0	8.5	18.7	10.1	118.0	52.0	39.8	92.5	1.7	0.8	0.1	6.0	0.2	3.4	6.4779
206472_s_at	NM_005078.1	immunoglobulin superfamily member	2.2	2.6	1.3	0.7	0.5	1.6	0.6	0.5	1.0	22.6	25.0	11.3	8.3	1.3	1.2	1.5	1.8	1.5	0.9	6.4334
212769_at	A0567426	WIN78	1.4	1.5	0.5	1.3	2.3	1.1	1.0	2.2	1.9	17.9	15.9	15.1	12.8	2.4	0.8	1.1	1.3	1.2	0.5	6.4271
204307_at	AB002295.1	FLJ11151	0.7	0.0	0.1	2.6	2.1	1.8	1.5	2.4	2.0	10.3	11.2	15.4	12.8	1.9	0.1	0.5	0.2	0.1	0.5	6.3478
203591_s_at	NM_000760.1	R Fc gamma receptor IIa (CD32)	0.1	0.0	1.0	0.1	0.2	2.3	0.6	2.4	1.0	220.3	187.2	134.9	112.1	0.2	0.8	0.2	25.5	0.1	0.2	6.2051
210210_at	AF181660.1	superoxide dismutase 2	0.9	1.1	1.8	1.8	1.9	1.1	1.9	1.7	2.0	11.1	7.0	13.7	14.1	1.4	1.3	0.9	1.6	1.1	0.6	6.172
218610_s_at	NM_018340.1	FLJ11151	1.5	1.2	1.2	1.2	1.8	3.3	3.2	2.6	1.8	25.2	23.3	17.9	21.8	0.5	0.6	0.4	3.6	0.4	0.6	6.112
203561_at	NM_021642.1	R	4.7	1.2	0.9	1.2	2.4	19.5	22.8	19.4	21.4	104.3	129.0	153.0	123.9	4.0	0.7	0.7	18.3	2.2	0.2	6.1015
216841_s_at	X15132.1		1.3	1.1	1.2	1.8	2.2	1.4	1.3	3.2	2.4	20.5	44.6	35.8	42.2	5.6	0.8	0.7	2.0	0.7	1.1	6.0724

## C. Neuophil (Ne)-selective transcripts (3/7).

Probe set	Accession #	Transcripts	MC, cord blood	MC, lung	Ba	Ba 2 (small)	Ba 3 (small)	Eo 1	Eo 2	Eo 3 (small)	Eo 4 (small)	Ne 1	Ne 2	Ne 3 (small)	Ne 4 (small)	pI	CD4	CD8	CD14	CD19	Fb	Ne S.I.
207624_s_at	NM_000328.1	retinitis pigmentosa regulator (RPGR)	0.0	0.6	1.1	2.0	1.2	1.1	1.2	2.1	2.8	7.1	7.0	13.6	15.1	0.2	1.2	0.4	0.9	0.7	0.3	6.0348
209850_s_at	BC005406.1	Cdc42 effector protein 2	0.2	0.2	1.3	0.2	1.0	0.2	0.4	0.5	0.4	13.2	9.6	6.7	8.7	0.2	0.2	0.2	0.6	0.4	1.6	5.9313
209396_s_at	NM_004994.1	matrix metalloproteinase 9	47.7	0.6	1.6	1.9	1.4	1.2	2.4	15.5	1.5	36.5	35.1	36.8	21.9	1.7	2.0	1.4	1.9	1.3	1.4	5.9311
215966_x_at	AA292874	glycerol kinase	1.2	0.2	0.6	0.1	1.2	0.2	1.0	1.2	1.2	6.6	10.2	7.3	7.4	0.2	0.1	0.2	1.3	0.5	0.0	5.9077
206925_at	NM_005668.1	sialyltransferase 8	3.1	1.2	2.1	2.5	2.0	1.4	3.1	1.6	1.6	21.7	33.3	6.8	11.4	0.4	0.9	1.6	2.6	1.2	0.2	5.8688
211764_s_at	BC005980.1	ubiquitin-conjugating enzyme E2D 1 phosphohydrolinosisl transfer protein (PITPN)	1.8	1.4	1.1	2.9	2.4	7.5	5.7	3.9	2.2	29.3	31.2	52.6	25.4	0.2	2.0	1.4	5.7	1.3	2.3	5.8143
201192_s_at	NM_006224.1	placental lactaine transporter	3.0	3.1	1.9	5.0	4.6	3.9	5.4	6.6	5.4	27.9	26.9	32.9	35.2	2.0	3.5	3.7	5.0	3.2	2.8	5.811
206921_s_at	U16120.1	ubiquitin c-terminal hydrolase related polypeptide	1.2	0.7	0.5	0.2	0.4	0.3	1.6	0.5	0.9	14.8	17.2	2.8	2.6	0.0	0.1	0.3	1.1	0.3	0.4	5.7909
209137_s_at	BC000263.1	Cardioembryonic antigen-related cell adhesion molecule 3 (CEACAM3)	3.6	4.1	2.0	2.6	1.9	1.5	0.9	2.7	0.9	25.0	24.5	37.6	29.7	3.5	5.0	2.5	3.5	2.7	3.0	5.7864
208052_x_at	NM_001815.1	insulin-like growth factor 2 receptor	1.7	1.4	2.9	2.7	1.9	3.0	2.6	2.8	2.1	14.3	16.5	20.0	13.7	2.5	1.3	2.3	2.8	2.5	1.6	5.7572
201393_s_at	NM_000876.1	FLJ10652	6.4	2.8	0.2	0.8	1.8	4.1	5.4	6.8	5.4	82.4	106.9	80.1	71.7	1.7	2.9	8.7	8.4	4.8	14.8	5.7104
218614_at	NM_018169.1	SEC14 (S. cerevisiae)-like 1	1.2	1.0	6.9	13.7	12.5	3.2	3.3	7.7	5.8	52.7	54.4	82.8	83.3	2.9	8.7	11.8	3.2	10.8	1.3	5.6442
202084_s_at	NM_003003.1	KIAA0615	5.7	2.5	12.8	28.8	22.6	20.6	18.7	35.5	29.5	130.7	129.7	135.6	177.9	19.2	4.1	3.5	11.5	7.7	11.8	5.6423
32069_at	AB014515	solute carrier family 22, member 4 (SLC22A4)	2.8	1.5	2.1	5.6	5.5	4.6	3.7	5.9	6.9	23.9	20.9	35.1	40.5	1.0	3.4	3.3	2.6	2.1	1.5	5.6348
205896_at	NM_003059.1	MD-2 protein	0.8	1.2	1.0	0.1	1.1	1.9	2.4	3.5	2.7	8.5	13.3	30.0	12.6	0.5	0.7	0.8	2.6	0.5	1.4	5.4612
206584_at	NM_015364.1	SEC14 (S. cerevisiae)-like 1	7.4	1.1	2.0	3.9	1.8	1.0	0.4	0.6	0.5	43.9	62.3	87.8	56.0	1.3	3.5	1.0	11.1	3.5	9.4	5.4459
202082_s_at	NM_003003.1	KIAA0329	1.0	0.3	3.6	2.5	2.2	15.5	5.4	12.3	8.4	40.2	57.3	54.9	60.9	3.8	0.8	1.3	2.7	3.3	2.4	5.4422
204308_s_at	NM_014844.1	casease 5	2.9	1.1	2.2	2.8	2.8	2.1	3.1	3.1	4.3	16.5	18.7	19.9	19.0	3.4	1.3	1.7	1.8	1.3	2.5	5.4369
207500_at	NM_004347.1	CD10, membrane metallo-endopeptidase	0.3	1.1	0.1	0.0	0.1	0.1	0.3	0.2	0.5	4.2	8.2	4.8	2.9	0.3	0.3	0.4	0.8	0.1	0.3	5.379
203435_s_at	NM_007287.1	adiponin	0.3	0.5	0.4	0.3	0.2	0.1	0.3	0.3	0.2	16.4	44.2	54.8	42.8	0.2	0.3	0.2	0.2	0.2	8.9	5.2591
205539_at	NM_006578.1	KIAA0615	0.4	0.5	2.0	1.4	0.8	1.0	1.1	1.0	1.1	8.4	8.9	6.0	10.1	1.0	1.3	0.4	1.5	0.7	1.1	5.2541
204601_at	NM_014664.1	long-chain 1 (FACL1)	1.9	1.2	1.3	3.2	2.3	3.0	2.7	3.7	3.0	12.9	12.8	20.2	20.0	0.1	2.2	2.6	1.3	1.9	1.0	5.2381
201963_at	NM_021122.2	fatly-eod-Coenzyme A ligase, long-chain 1 (FACL1) CXCR1 interleukin 8 receptor, alpha	2.9	2.1	5.0	19.9	33.4	6.6	3.8	10.3	6.1	58.8	86.6	92.2	80.2	0.1	1.1	1.1	10.8	1.5	2.4	5.2374
207064_s_at	NM_009590.1	GPR	0.7	0.1	0.9	0.9	0.8	0.8	0.8	0.9	1.2	4.3	4.7	4.0	6.6	0.8	0.5	0.8	0.5	0.8	0.3	5.1905
220005_at	NM_023914.1	P2YX purinergic receptor GPR86 for UDP-glucose	0.6	0.0	0.1	0.5	0.1	19.7	9.6	25.1	17.3	76.5	77.1	100.7	98.6	1.9	0.1	0.2	12.3	0.6	0.0	5.1686
211395_x_at	U09940.1	Fc gamma receptor IIc3	4.6	0.3	7.3	9.7	15.1	9.7	19.5	4.4	6.6	115.0	140.3	42.9	38.9	3.0	1.4	0.6	14.0	7.2	1.0	5.1401
201780_s_at	NM_007282.1	ring finger protein 13 (RNF13)	4.4	2.8	3.5	9.2	6.6	6.8	6.2	8.9	7.1	27.1	36.6	52.5	35.7	0.8	4.1	3.7	7.2	7.2	4.8	5.1305
209864_at	AB045118.1	GSK-3 binding protein FRAT2 pellino (Drosophila) homolog 1 (PEL11)	2.8	1.3	4.4	9.2	8.0	13.4	16.9	27.3	22.6	93.2	97.2	100.6	104.2	1.3	1.9	2.9	10.2	2.5	1.0	5.1047
218319_at	NM_020651.2	phorbol	3.4	2.9	5.9	17.5	33.5	17.7	11.7	12.6	15.1	64.9	88.3	73.0	80.2	2.4	6.3	2.9	13.8	12.8	1.1	5.0403
206632_s_at	NM_004900.1	phorbol	0.6	1.1	1.0	1.2	2.6	1.3	0.8	3.9	0.5	19.6	11.1	30.8	0.5	1.5	0.2	0.4	0.4	1.0	1.2	5.0277
209990_s_at	NM_030938.1	DKFZp661133	11.7	6.2	4.6	18.5	12.5	5.0	3.3	8.2	4.9	115.5	117.2	125.3	122.5	2.6	5.3	4.2	24.1	4.4	8.3	4.9858
221653_x_at	BC004395.1	apolipoprotein L	0.7	2.8	0.6	2.1	1.6	2.0	0.4	1.8	1.1	8.0	3.9	12.7	5.2	0.2	0.9	0.4	1.4	1.1	0.4	4.9332
204748_at	NM_000983.1	COX2 prostaglandin-endoperoxide synthase 2	6.5	16.2	0.6	2.4	2.0	4.5	2.3	3.4	3.4	35.8	44.1	44.6	91.8	0.4	0.6	0.2	4.3	0.3	0.5	4.9206
210423_s_at	L32185.1	integral membrane protein	2.0	0.2	1.4	1.6	1.3	1.3	2.2	1.5	2.0	85.0	78.5	75.2	52.9	1.9	0.4	1.9	14.7	1.0	1.0	4.8845
206429_at	NM_005242.2	PAR2 proteinase activated receptor-2	0.8	0.8	0.9	0.2	0.9	0.9	1.1	0.2	0.8	11.8	15.1	4.1	4.1	1.3	1.5	0.2	1.5	0.3	0.7	4.8608
213352_at	A1934469	KIAA0779	0.6	0.9	1.2	1.5	1.2	1.2	1.5	1.5	2.2	8.4	6.0	8.7	7.7	1.6	0.9	1.5	1.0	1.3	0.8	4.8373
201888_s_at	U81379.3	interleukin-13 receptor	0.1	0.6	0.3	0.2	0.0	1.7	2.7	1.7	2.0	8.6	19.0	15.0	13.9	0.4	0.4	0.3	2.9	1.3	1.3	4.746

Figure 6F

## C. Neutrophil (Ne)-selective transcripts (4/7)

Probe set	Accession #	Transcripts	MC, cord blood	MC, lung	Ba 1	Ba 2 (small)	Ba 3 (small)	Eo 1	Eo 2	Eo 3 (small)	Eo 4 (small)	Ne 1	Ne 2	Ne 3 (small)	Ne 4 (small)	pI	CD4	CD8	CD14	CD19	Fb	Ne S.I.
204780_s_at	AA164751	R CD95, Fas, APO-1	1.4	1.4	7.2	14.0	11.5	6.6	6.7	9.3	6.6	45.3	36.6	65.5	51.6	1.3	5.6	4.6	3.6	2.6	9.7	4.7254
209310_s_at	U25804.1	Ich-2 cysteine protease phosphatidylinositol glycan class B (PICB)	2.5	1.9	2.1	7.7	7.0	1.4	1.3	1.3	1.4	19.1	17.5	36.7	23.5	2.9	4.1	4.5	4.9	3.9	2.2	4.6817
205452_at	NM_004855.1	FLJ20950	2.3	2.7	2.3	6.4	7.7	2.3	1.4	3.0	3.0	16.3	17.6	22.2	39.3	1.7	2.0	2.9	2.8	3.5	2.2	4.6577
218298_s_at	NM_024952.1	swine acetylneuraminylase	3.1	3.3	5.4	8.1	7.2	5.7	5.7	8.8	9.4	37.2	23.4	37.3	39.1	0.6	1.7	3.1	5.8	2.3	2.7	4.6558
221210_s_at	NM_030769.1	chromosome 1 open reading frame 12, clone MGC:12484	3.8	1.2	0.8	1.2	1.4	3.0	4.7	3.2	4.6	20.4	23.6	23.5	18.3	0.6	0.1	0.3	4.6	0.5	0.1	4.6378
221497_x_at	BC005369.1	fertilin, light polypeptide-like 1	3.0	2.4	4.3	5.7	5.9	3.3	7.6	7.9	5.4	29.3	32.4	24.3	21.5	1.8	3.1	2.9	2.9	1.9	2.0	4.6333
204668_at	AL031670	guanine nucleotide binding protein 10 (GNG10)	0.8	0.5	1.8	1.0	1.2	0.3	1.5	1.7	0.9	8.4	8.1	7.0	6.5	1.4	1.3	1.0	1.5	0.5	1.6	4.614
201921_at	NM_004125.1	peroxisomal acyl-coenzyme A oxidase	7.1	5.4	2.6	6.7	6.5	11.7	11.4	20.6	15.3	45.5	87.5	81.3	57.1	0.8	2.7	3.0	8.4	3.2	12.4	4.5644
209600_s_at	S69189.1	formyl peptide receptor 1	2.9	1.7	2.8	5.3	4.7	1.4	1.0	1.2	1.3	15.0	17.7	21.4	21.2	0.4	1.0	0.8	2.1	0.7	1.5	4.5552
205119_s_at	NM_002029.1	pre-B-cell colony-enhancing factor	4.1	1.4	11.2	26.6	32.7	14.0	11.1	4.2	6.0	288.2	315.8	274.7	252.9	3.6	1.3	0.7	62.6	1.1	0.5	4.505
217738_at	BF575514	DKF Zp564M2422	5.7	0.9	7.4	24.1	34.9	7.5	4.6	5.1	3.9	73.4	87.0	89.9	79.9	2.2	1.7	1.6	10.1	1.7	2.8	4.4839
205078_at	AL050388.1	numb (Drosophila) homolog	0.0	0.1	0.0	0.1	0.4	0.9	0.5	0.8	0.3	7.1	12.9	4.5	7.9	0.1	0.5	0.5	1.7	0.1	0.1	4.4343
207545_s_at	NM_003744.1	heat shock 70kD protein 6 (HSP70B)	0.7	1.4	1.1	2.5	2.4	2.7	1.8	2.9	1.2	7.2	11.2	10.5	7.4	0.8	0.5	0.5	1.6	1.1	1.2	4.3728
213418_at	NM_002155.1	pulvinar nuclear protein (LOC51307)	1.1	0.4	0.7	1.5	1.6	25.3	28.8	10.5	17.0	104.0	91.6	70.0	70.8	0.5	1.1	1.1	12.8	4.7	0.5	4.3655
218023_s_at	NM_016605.1	Similar to metaxin 1	5.7	3.8	6.6	13.0	12.6	8.5	10.3	13.0	10.9	40.1	39.7	47.0	59.7	3.0	4.4	5.9	7.0	6.0	6.6	4.3383
210386_s_at	BC001906.1	CD120a, TNF- $\alpha$ p55	6.2	1.9	2.7	5.4	4.0	1.4	2.2	1.8	3.6	19.5	15.8	23.4	23.8	2.5	3.6	2.6	4.1	2.6	4.7	4.3318
207643_s_at	NM_001065.1	B-cell CLL/lymphoma 6 (BCL6)	1.8	1.6	0.9	1.3	1.4	6.3	7.4	8.5	9.0	81.1	83.6	68.6	65.6	1.3	2.2	5.9	17.4	0.6	16.0	4.2798
203140_at	NM_001706.1	ubiquitin 1	8.2	2.9	9.1	13.5	19.8	23.5	16.7	28.7	33.1	99.1	107.8	115.8	101.1	2.2	3.4	3.4	23.4	8.7	6.5	4.2767
207253_s_at	NM_016936.1	pre-B-cell leukemia transcription factor 2	3.2	2.8	2.9	4.4	5.0	3.8	2.6	3.8	3.6	16.7	20.0	14.2	17.8	2.3	2.5	2.5	2.2	2.4	1.8	4.2556
202875_s_at	BE397715	FLJ22557	2.0	1.4	0.1	0.1	0.2	2.5	3.6	2.1	1.5	11.8	15.4	6.8	7.5	0.8	1.7	1.9	1.1	1.3	0.7	4.2425
218791_s_at	NM_024713.1	Ursupin-beta	1.2	0.7	2.5	2.7	1.8	0.9	1.5	1.6	1.0	6.9	8.7	13.2	11.2	1.4	1.0	0.5	1.3	0.8	1.2	4.2114
211862_x_at	AF015451.1	bromodomain adjacent to zinc finger domain, 1A	3.5	2.8	16.8	9.7	10.1	5.6	10.2	7.7	7.1	65.7	67.7	38.1	37.9	3.1	6.8	8.7	10.1	6.9	2.0	4.2001
217986_s_at	NM_013448.1	niban	3.5	3.0	3.5	9.2	8.4	6.1	8.5	14.5	13.1	39.0	35.1	43.5	51.6	2.5	5.9	6.5	7.0	5.0	1.7	4.1976
217966_s_at	NM_022083.1	KIAA0993	4.1	1.9	6.4	7.4	9.0	24.2	14.6	25.6	11.8	51.9	105.3	76.2	80.0	0.9	3.3	3.8	3.2	2.0	8.2	4.1858
212602_at	A1806395	CASP8 and FADD-like apoptosis regulator (CFLAR)	2.3	3.5	0.4	0.9	1.1	0.8	0.6	0.4	0.8	17.1	18.1	12.9	13.4	1.5	0.5	0.3	3.6	0.8	2.6	4.1806
208465_x_at	NM_003879.1	gp180-carboxypeptidase D-like enzyme	3.2	2.5	19.2	9.8	9.9	6.2	13.0	8.1	8.3	70.8	89.7	33.6	41.4	3.5	6.4	8.4	11.5	6.6	2.0	4.1719
201942_s_at	D85390.1	FLJ13409	0.6	1.7	0.6	1.3	1.7	1.6	7.0	2.4	2.6	15.9	23.8	6.8	6.1	0.5	0.8	1.3	2.5	0.5	2.6	4.1525
209333_s_at	NM_024617.1	glycerol-3-phosphate dehydrogenase 1	2.1	2.0	9.6	14.2	14.0	7.1	7.2	10.9	12.5	38.1	37.3	81.5	57.8	1.9	3.1	4.8	6.2	3.8	3.0	4.1025
221764_at	AL574186	Toll-like receptor 6	6.3	4.4	16.5	16.6	15.0	10.4	15.6	21.9	22.7	80.9	99.2	46.3	60.3	9.5	6.9	9.4	5.7	9.4	2.5	4.0745
207446_at	NM_006088.1	chromosome 6 open reading frame 76	0.5	0.5	0.7	1.5	0.8	0.8	0.9	1.2	0.8	7.6	11.8	7.2	8.7	0.1	0.9	0.9	2.1	1.2	0.6	4.0697
219748_at	NM_024807.1	FLJ10298	0.2	0.3	0.3	0.4	0.6	1.9	2.6	1.6	1.6	9.1	9.1	6.7	6.4	0.2	0.3	0.6	0.5	1.1	0.0	4.0619
220945_x_at	NM_018050.1	KIAA0650	1.0	1.4	0.5	0.7	0.7	1.1	0.6	1.5	1.0	6.0	10.6	13.6	11.0	1.1	0.5	0.3	0.9	0.6	2.6	4.057
212577_at	AA668754	RIKEN cDNA 5830420C20	1.9	1.3	6.4	8.0	9.9	10.1	24.0	8.1	9.4	74.0	98.6	42.2	57.4	4.4	10.8	9.5	7.5	16.0	3.2	4.0417
221732_at	AK026161.1	apoptosis-associated tyrosine kinase	2.6	0.7	3.4	10.5	8.8	5.0	6.0	10.7	10.9	27.6	31.6	30.8	34.7	0.3	0.4	1.8	2.5	1.6	4.6	4.041
205986_at	NM_004920.1	acyl-Coenzyme A oxidase 1	1.6	1.3	0.7	1.0	0.5	0.3	0.3	1.4	1.0	10.5	15.8	13.3	15.2	3.2	1.0	0.5	3.4	0.9	0.4	4.0322
213501_at	T62985	palmitoyl	1.3	1.1	2.0	2.6	2.6	1.3	0.9	1.2	0.6	8.5	11.5	12.4	7.5	0.1	1.1	0.3	1.8	0.5	1.1	4.0194
204542_at	NM_006456.1	sialyltransferase (ST6M)	0.4	0.2	1.5	0.3	0.2	3.4	3.9	4.5	3.2	13.0	13.4	21.0	13.4	0.7	0.7	0.3	1.4	0.3	0.6	4.016

Figure 6C

## C. Neutrophil (Ne)-selective transcripts (5/7).

Probe set	Accession #	Transcripts	MC, cord blood	MC, lung	Ba	Ba 2 (small)	Ba 3 (small)	Eo 1	Eo 2	Eo 3 (small)	Eo 4 (small)	Ne 1	Ne 2	Ne 3 (small)	Ne 4 (small)	pI	CD4	CD8	CD14	CD19	Fb	Ne S.I.
204071_s_at	NM_005802.1	tumor protein p53-binding protein	1.4	1.6	1.1	3.0	2.9	3.7	2.3	2.6	2.2	10.5	12.8	8.0	11.9	1.5	2.2	2.2	1.4	2.2	2.1	4.0148
210594_x_at	AF239756.1	myelin protein zero-like 1	1.2	0.5	0.6	1.5	1.2	0.1	0.4	0.8	1.9	15.3	13.9	7.1	10.9	0.3	0.2	0.6	1.0	0.7	2.8	3.9778
203063_at	NM_014634.1	protein phosphatase 1F (PP2C domain containing)	0.5	0.4	1.4	3.3	3.0	4.0	6.0	6.1	10.0	33.1	22.2	29.6	31.8	0.3	2.9	1.2	7.3	1.5	1.8	3.9764
201392_s_at	BG031974	insulin-like growth factor 2 receptor	1.7	0.7	0.1	0.0	0.1	2.6	3.0	1.9	1.5	51.1	59.1	12.0	15.0	1.1	1.2	4.0	3.8	2.2	7.0	3.9602
221477_s_at	BF575213	MGC5618	2.9	1.4	3.4	4.3	9.0	-4.2	4.2	4.2	4.2	56.8	63.6	36.1	46.6	7.9	3.2	1.2	12.6	2.7	2.1	3.9562
206756_at	NM_019886.1	carbohydrate (N-acetylglucosamine 6-O)sulfatase 7	0.2	0.1	0.1	0.0	0.1	0.1	0.1	0.1	0.1	5.0	3.9	3.5	10.5	0.1	1.3	1.0	1.0	0.2	0.5	3.9516
204994_at	NM_002463.1	myxovirus (influenza) resistance 2 (MX2)	1.3	2.3	5.4	7.8	8.2	9.2	11.6	15.2	12.3	49.8	46.6	77.6	80.8	2.4	7.5	6.0	15.6	4.8	1.8	3.9478
201943_s_at	NM_001304.2	carboxypeptidase D	0.9	0.9	0.5	2.1	3.6	1.7	7.6	7.2	4.6	16.4	21.3	18.7	15.2	0.7	1.0	1.7	3.3	0.4	3.8	3.8926
216252_x_at	Z70519.1	CD95, Fas, APO-1	0.3	0.8	4.3	2.5	1.1	1.8	4.7	1.8	1.7	18.5	31.2	10.3	8.4	2.2	3.8	2.4	1.9	1.4	3.9	3.8691
203086_at	NM_014863.1	B cell RAG associated protein (BRAG)	1.3	3.9	0.9	1.2	1.0	10.6	10.2	13.1	20.2	57.0	65.9	95.2	86.9	1.9	0.1	0.0	19.3	4.2	5.9	3.8667
212479_s_at	AL050139.1	FLJ13910	1.7	1.6	2.1	2.5	2.6	2.4	2.5	3.5	1.7	9.0	10.1	8.8	9.8	1.1	2.3	2.4	2.2	1.9	0.9	3.8422
209571_at	U03644.1	receptin	0.7	0.2	1.6	3.3	2.7	2.2	1.3	2.6	2.7	6.8	7.8	12.8	10.9	0.8	1.0	1.1	1.2	1.5	1.1	3.8367
211317_s_at	AF041461.1	CASP8 and FADD-like apoptosis regulator	1.6	1.8	9.5	3.6	4.0	3.7	6.8	3.2	2.8	33.1	44.8	15.2	17.6	2.4	4.7	6.5	5.7	4.9	1.1	3.8332
209732_at	BC005254.1	C-type (calcium dependent, carbohydrate-recognition domain)	8.1	5.9	10.0	18.6	23.8	9.0	10.0	8.9	7.3	72.9	77.0	99.7	75.5	4.1	14.4	21.2	10.2	16.4	1.3	3.8003
201779_s_at	AF070558.1	lectin, superfamily member 2	14.8	5.9	13.0	13.3	13.9	21.8	27.0	25.3	13.1	88.2	108.1	116.5	81.8	8.0	9.6	11.3	25.7	15.7	8.5	3.7993
212441_at	D85985.2	RZF	5.4	2.9	3.5	9.8	10.3	8.0	6.9	11.5	11.3	31.9	30.1	30.8	49.8	2.5	2.0	4.0	5.9	2.1	4.9	3.7868
206920_at	NM_003043.1	KIAA0232	1.2	1.4	0.9	0.2	0.2	1.1	5.2	0.7	1.4	33.1	26.7	2.7	4.0	0.3	0.1	0.4	-2.8	0.1	0.5	3.7836
213596_at	AL050391.1	soluble carrier family 6, member 6 (SLC6A6)	0.7	0.7	2.3	3.6	3.0	1.2	1.2	1.1	1.2	10.6	10.9	12.5	9.9	2.2	1.1	2.0	1.5	0.7	0.3	3.7615
209508_x_at	AF005774.1	DKFZ586A181	1.7	2.7	10.8	7.6	11.5	4.9	6.3	8.0	8.4	37.0	34.8	34.7	40.8	2.7	4.0	5.1	8.3	3.4	1.3	3.7451
218115_at	NM_018154.1	protein (clap)	0.9	2.2	2.4	1.5	0.9	1.8	2.1	1.3	1.1	10.5	9.1	6.7	7.7	1.1	1.2	2.2	2.1	1.7	1.5	3.7435
215652_at	AK024382.1	FLJ10604	0.2	0.1	2.0	0.3	1.6	0.3	0.3	1.2	0.7	5.5	4.5	3.4	2.5	0.1	0.3	1.0	0.9	0.2	0.6	3.7249
212581_at	AA349595	FLJ14320	10.0	6.1	10.2	12.4	11.4	18.7	14.9	12.1	10.0	66.3	60.0	47.6	37.1	4.0	8.7	9.9	13.9	5.9	10.2	3.6962
204166_at	NM_014963.1	RAB8 interacting protein 1	3.6	0.4	1.1	0.0	0.1	1.0	1.3	0.1	0.8	11.8	12.5	4.0	2.9	0.3	0.9	1.7	1.7	1.2	0.2	3.6908
221874_at	AB037745.1	KIAA0963	0.3	0.3	0.7	1.1	0.3	0.8	0.8	0.7	0.5	9.1	5.1	5.1	1.2	0.9	1.1	0.7	0.5	0.6	0.4	3.6808
217207_s_at	AK025287.1	KIAA1324	1.2	1.1	1.4	2.1	1.7	1.2	1.9	0.6	2.4	10.9	3.4	7.2	6.1	1.5	1.7	1.6	0.9	1.5	1.3	3.6795
212579_at	AA868754	butyrophilin like receptor	1.3	1.8	5.3	9.8	15.5	7.3	7.8	11.3	8.3	32.8	42.9	40.0	39.7	2.0	5.4	5.7	3.1	10.5	2.2	3.6784
212657_s_at	AW083357	KIAA0650	48.8	2.3	0.9	0.5	0.6	-2.1	0.9	1.5	1.3	35.2	37.0	48.2	35.5	0.6	0.8	0.3	9.3	0.4	0.6	3.6759
202392_s_at	NM_014338.1	IL-1 receptor antagonist IL-1RA	3.4	2.7	6.2	11.7	6.8	3.4	4.7	5.4	4.7	32.8	31.0	22.0	32.3	0.8	1.6	1.4	4.2	1.4	1.2	3.6753
206177_s_at	NM_000045.2	phosphatidylserine decarboxylase	0.5	1.3	2.2	0.4	0.6	0.9	0.8	7.2	0.7	3.9	4.3	8.1	5.0	1.1	0.1	0.4	0.6	0.7	0.0	3.6722
200706_s_at	NM_004862.1	arginase (ARG1)	31.2	39.0	20.7	64.6	62.5	15.6	13.4	31.8	21.7	173.2	148.5	172.0	150.2	8.5	13.3	42.7	14.3	16.7	18.2	3.6696
212478_at	AL050139.1	LPS-induced TNF-alpha factor (PIG7)	0.1	0.1	0.2	2.3	3.5	1.4	0.8	1.5	1.0	3.7	3.0	4.8	6.5	0.1	0.3	1.1	0.6	0.4	0.5	3.6623
218660_at	NM_003494.1	FLJ13910	2.5	0.5	1.5	0.2	0.2	1.7	0.2	2.6	1.1	48.5	51.8	44.5	20.4	3.3	1.2	1.7	10.6	0.2	1.3	3.6616
211982_x_at	AL546600	dysferlin	9.8	6.7	14.9	31.8	27.8	24.6	24.0	34.0	24.0	107.2	101.1	86.6	90.2	6.6	17.5	17.4	9.6	11.5	7.7	3.6408
202748_at	NM_004120.2	expofin 6	2.4	5.3	3.7	9.0	7.4	3.3	2.1	3.0	3.3	28.1	35.2	45.0	24.8	4.2	7.3	9.0	6.3	1.9	3.7	3.6111
220088_at	NM_001736.1	guanylate binding protein 2	2.2	2.3	15.4	24.6	24.8	17.1	15.6	9.8	12.0	90.5	104.5	84.4	91.1	2.3	1.2	0.5	25.6	1.0	0.4	3.6036
202890_at	T62571	C5a receptor	0.9	0.1	0.7	1.4	1.1	0.1	0.0	0.2	0.1	2.5	3.1	3.2	7.1	0.0	0.1	0.4	0.1	0.1	0.0	3.6032
220987_s_at	NM_030952.1	microtubule-associated protein 7	1.4	0.3	3.9	4.9	4.7	9.6	9.3	14.1	11.7	43.0	35.6	57.8	57.6	5.3	4.7	4.8	11.1	13.3	2.0	3.5748
		DKFZP434J037																				



## C. Neutrophil (Ne)-selective transcripts (6/7).

Probe set	Accession #	Transcripts	MC, cord blood	MC, lung	Ba	Ba 2 (small)	Ba 3 (small)	Eo 1	Eo 2	Eo 3 (small)	Eo 4 (small)	Ne 1	Ne 2	Ne 3 (small)	Ne 4 (small)	pl	CD4	CD8	CD14	CD19	Fb	Ne S.I.
215719_x_at	NM_003853.1	interleukin 18 receptor accessory protein (IL18RAP)	5.9	0.9	2.2	3.4	4.1	7.2	1.6	2.8	1.7	13.4	9.7	20.9	5.6	2.4	2.8	3.1	0.4	1.8	0.3	3.5722
215719_x_at	X83493.1	CD95, Fas, APO-1	1.0	0.6	3.1	2.7	1.6	2.2	5.2	1.8	1.7	19.0	31.9	11.4	9.4	1.0	4.5	2.2	1.6	1.1	4.4	3.5657
218404_at	NM_013322.1	sorbing nexin 10	4.9	1.2	2.6	5.0	3.7	0.7	0.1	2.1	0.7	28.5	31.8	34.8	33.8	0.3	1.2	1.9	9.0	8.5	0.3	3.563
219394_at	NM_024419.1	phosphatidylglycerophosphate synthase (PGS1)	3.4	3.0	1.7	4.2	3.5	2.4	3.8	6.1	9.2	17.2	16.9	17.5	16.3	1.0	2.1	2.6	2.4	1.5	1.7	3.5544
216913_s_at	AK021460.1	KIAA0690	0.1	0.3	0.1	0.1	0.1	1.9	2.5	2.3	2.8	8.9	8.3	7.5	10.9	0.1	0.1	0.2	2.5	0.1	0.0	3.5402
205118_at	M60626.1	formylpeptide receptor 1	0.1	0.2	0.8	0.1	0.1	0.1	0.4	0.6	0.1	3.9	7.0	3.2	7.8	0.2	0.1	0.1	1.4	0.1	0.0	3.5295
210564_x_at	AF009619.1	FLAME-1- <i>delta</i>	1.4	1.5	5.3	6.6	7.0	4.3	4.2	5.9	3.5	21.2	30.3	18.4	19.6	2.1	2.9	4.0	4.6	3.0	1.8	3.5148
213607_x_at	BE551347	KIAA0134	1.3	1.3	2.9	2.0	1.7	8.7	15.8	3.5	4.3	42.7	42.5	11.1	15.3	0.6	1.3	1.9	6.2	1.7	0.9	3.514
203888_at	NM_000361.1	thrombomodulin	0.9	0.6	0.1	0.1	0.3	0.2	0.4	0.8	0.1	6.1	8.4	4.6	0.2	0.3	0.3	0.1	0.6	0.5	0.1	3.5126
210233_at	AF167343.1	interleukin-1 receptor accessory protein (IL1RAP)	0.5	0.1	0.0	0.1	0.6	0.8	0.4	0.6	0.7	1.8	3.0	2.0	2.3	0.6	0.0	0.0	0.0	0.0	0.3	3.5023
204959_at	NM_002432.1	myeloid cell nuclear antigen	1.2	0.6	24.2	50.0	26.2	17.5	17.9	49.8	22.3	249.8	290.2	186.0	217.0	3.4	1.6	0.6	66.6	2.5	0.0	3.4903
217967_s_at	AF288391.1	niban	6.3	3.7	16.3	42.4	35.9	27.9	29.5	43.0	30.9	107.4	115.3	117.9	110.3	2.6	7.5	9.9	4.9	3.4	20.4	3.4847
221763_at	A1694023	thyroid hormone receptor interactor 8	0.8	1.5	1.9	4.6	5.5	5.5	6.9	9.9	9.0	26.3	32.9	34.0	42.7	1.1	3.7	4.1	5.1	9.8	3.0	3.4777
207857_at	NM_006866.1	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 2 (LILRA2)	0.4	0.5	3.6	8.5	5.3	4.5	4.9	1.6	6.3	33.5	34.3	46.2	50.8	1.8	0.0	0.1	11.6	0.5	0.1	3.4773
220740_s_at	NM_005135.1	solute carrier family 12 member 6 (SLC12A6)	1.6	1.0	2.5	3.3	3.4	3.5	5.6	3.2	3.2	12.6	19.0	10.7	14.4	4.0	2.9	2.2	2.9	3.5	0.8	3.4722
217739_s_at	NM_005746.1	pre-B-cell colony-enhancing factor	7.1	1.7	9.9	48.0	61.0	18.9	13.9	12.9	9.3	112.4	120.5	90.8	93.4	1.2	2.3	1.4	17.6	2.1	3.1	3.4242
205041_s_at	NM_000607.1	orostomucoid 1 (ORM1)	0.3	1.0	0.4	0.1	0.1	0.0	0.1	1.0	0.1	2.6	3.6	2.7	0.4	0.1	0.2	0.1	0.5	0.0	0.1	3.4189
214784_x_at	BE566299	expartin 6	7.4	5.0	10.0	23.7	23.9	13.0	16.7	23.3	20.5	60.3	87.8	57.2	60.8	2.9	8.7	7.8	6.6	5.9	5.4	3.4155
217965_s_at	AA102574	bromodomain adjacent to zinc finger domain, 1A	1.5	1.4	1.8	2.6	3.8	7.4	5.1	7.3	4.7	16.9	19.2	22.1	24.2	2.7	2.5	2.3	3.5	2.4	0.9	3.3999
212598_at	A1808395	KIAA0593	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	5.5	7.3	3.1	3.2	0.2	0.1	0.0	1.0	0.1	1.3	3.3933
219053_s_at	NM_017966.1	FLJ20847	2.6	2.0	1.9	2.3	2.3	2.6	2.1	3.0	2.8	11.3	7.8	22.2	34.1	1.8	0.5	0.9	4.7	1.3	2.9	3.3686
217475_s_at	AC002073	PAC clone RP3-515N1	0.6	0.5	0.6	0.2	0.4	1.3	1.3	0.5	1.2	5.9	9.8	1.6	1.4	0.7	0.3	0.1	0.5	0.7	0.2	3.3448
46323_at	AL120741	Ca2+-dependent endoplasmic reticulum nucleoside diphosphatase	4.4	3.2	4.2	8.3	7.2	5.3	6.7	11.4	7.9	20.0	21.5	33.9	26.3	2.5	2.8	3.6	4.3	3.4	5.0	3.3028
21965_s_at	NM_015046.1	KIAA0625	2.7	3.1	3.3	8.5	8.3	4.9	5.8	7.4	7.5	19.5	18.5	18.7	27.8	2.2	3.9	3.4	4.6	5.8	2.6	3.3019
203628_at	NM_000875.2	insulin-like growth factor 1 receptor LIM domain kinase 2 (LIMK2), transcript variant 2a	0.5	0.1	3.7	3.0	4.0	6.8	4.9	2.7	5.8	18.8	23.4	6.8	20.6	1.6	0.1	2.8	2.4	2.0	3.5	3.2989
202193_at	NM_005569.2	lysosomal-associated membrane protein 2 (LAMP2)	1.8	1.5	1.9	5.6	5.6	6.4	4.8	11.3	8.9	17.0	20.5	36.5	28.2	0.1	1.3	1.1	0.6	0.5	0.8	3.2887
203042_at	NM_002294.1	FLJ10357	2.4	3.1	1.1	1.7	1.3	5.9	6.4	12.4	10.7	21.3	27.0	44.1	35.4	0.8	0.6	0.5	3.2	0.8	9.4	3.282
220326_s_at	NM_018071.1	sperm associated antigen 9	5.1	4.5	1.9	1.2	1.9	6.3	8.9	5.2	8.5	25.3	28.1	19.2	21.0	0.9	0.1	0.7	6.4	0.1	4.1	3.2759
212470_at	AB011088.1	clone 6 immunoglobulin-like transcript 5	4.0	2.9	3.3	6.3	7.2	4.5	4.0	4.7	4.9	13.2	17.0	18.1	24.0	1.2	2.5	2.2	3.9	3.0	5.4	3.2688
211133_x_at	AF009643.1	DKFZp434C0328	1.9	1.4	0.8	1.5	1.3	3.1	2.7	3.8	2.1	42.1	42.2	27.0	25.1	2.7	0.9	0.5	10.2	0.4	0.2	3.2526
219313_at	NM_017577.1	G protein-coupled receptor GPR77	0.0	0.8	0.2	0.0	0.4	0.2	0.1	0.1	0.0	3.8	3.7	3.1	5.6	0.2	0.1	0.1	0.0	1.2	0.1	3.2404
221149_at	NM_018485.1	5, 10-methylenetetrahydrofolate synthetase	0.2	0.1	0.8	0.7	1.2	0.7	0.9	0.9	0.6	3.3	3.2	4.2	2.9	0.0	0.3	0.2	1.0	0.1	0.3	3.2282
203433_at	NM_006441.1	FADD-like apoptosis regulator	1.4	1.8	1.5	2.5	1.6	3.1	4.2	3.5	3.1	15.8	11.4	9.6	9.0	1.6	1.8	1.9	2.9	1.7	1.5	3.2181
214486_x_at	AF041459.1		1.9	2.1	10.7	5.0	6.5	4.2	5.3	4.3	6.0	26.3	18.2	25.3	24.2	2.4	3.7	5.0	5.3	2.3	1.9	3.2114

## C. Neutrophil (Ne)-selective transcripts (7/7).

Probe set	Accession #	Transcripts	MC, cord blood	MC, lung	Ba 1	Ba 2 (small)	Ba 3 (small)	Eo 1	Eo 2	Eo 3 (small)	Eo 4 (small)	Ne 1	Ne 2	Ne 3 (small)	Ne 4 (small)	pI	CD4	CD8	CD14	CD19	Fb	Ne S.I.
209222_s_at	BC000296.1	oxysterol binding protein-like 2	1.3	0.2	2.7	8.8	8.0	5.4	5.4	7.7	7.3	17.2	18.4	22.3	23.9	0.9	2.3	3.4	2.8	2.0	1.3	3.1877
202334_s_at	AA877765	ubiquitin-conjugating enzyme E2B mitogen-activated protein kinase kinase 4	3.3	3.4	4.8	15.5	12.1	5.3	7.2	14.7	12.8	20.9	25.6	43.6	38.1	4.0	4.5	3.9	2.5	4.9	4.6	3.1871
203266_s_at	NM_003010.1	FLJ10357	3.7	2.4	4.9	8.2	6.3	2.5	4.8	6.8	5.0	14.7	15.2	27.4	26.9	2.8	2.4	2.8	2.7	2.3	2.7	3.1804
58780_s_at	R42449		4.5	5.4	1.5	3.9	3.0	7.8	9.6	12.8	16.4	28.0	27.6	46.7	44.1	1.2	0.6	0.1	6.5	0.2	5.7	3.1803
210582_s_at	AL117466.1	LIM domain kinase 2	3.8	1.9	4.3	5.1	4.8	8.7	10.3	10.8	9.4	33.9	36.5	30.8	23.8	1.3	1.7	1.8	1.9	0.9	1.4	3.1609
214766_s_at	AL080144.1	TM6SF2	1.3	0.2	2.0	3.1	4.2	1.9	1.4	2.1	2.4	9.4	9.5	9.9	11.3	3.2	1.3	0.8	0.5	1.0	1.3	3.1414
202266_at	NM_016614.1	TRAF and TNF receptor-associated protein (AD022)	9.8	6.2	9.4	23.7	20.9	8.6	9.9	16.5	14.0	36.1	56.5	64.5	57.5	4.5	7.7	9.4	5.3	8.2	6.3	3.1402
203278_s_at	NM_016621.1	BRAF35/HDAC2 complex (80 kDa) transmembrane	2.1	2.8	2.7	14.8	11.0	5.7	5.0	7.4	4.9	21.0	16.6	31.0	30.6	0.1	3.0	4.5	3.1	2.7	3.0	3.1382
207291_at	NM_024081.1	gamma-carboxyglutamic acid protein 4	0.1	1.2	1.3	1.4	1.1	0.9	0.2	0.4	0.2	3.8	7.9	4.5	8.5	0.2	0.8	0.1	1.9	1.1	0.4	3.1336
213229_at	BF590131	Dicer1, Dcr-1 homolog (Drosophila)	8.5	4.5	19.5	12.9	15.4	15.9	9.7	19.1	16.0	35.2	39.0	61.4	69.4	6.2	5.9	7.3	15.2	12.2	5.0	3.1306
204204_at	NM_001880.1	solute carrier family 31	1.7	1.7	1.3	0.3	0.8	1.7	0.9	2.3	1.2	22.6	23.8	31.3	36.0	2.0	1.2	1.2	8.9	0.2	0.4	3.1262
201364_s_at	AF242521.1	ornithine decarboxylase antizyme domain 17B immunoglobulin-like transcript	8.3	7.3	4.4	2.2	1.9	11.5	21.9	8.0	7.7	61.9	59.1	21.0	27.7	2.2	5.1	6.3	12.2	6.2	9.6	3.1253
210784_x_at	AF009634.1	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog (LYN)	1.4	0.1	2.1	1.2	2.4	2.5	2.2	2.8	2.1	52.1	48.8	31.8	36.3	0.8	0.2	0.2	13.3	0.3	0.2	3.1236
202625_at	A1358412	hypothetical protein MGC26706	6.9	6.9	5.0	18.2	14.9	20.7	21.7	27.7	28.6	74.7	76.3	77.5	75.7	7.5	1.7	0.9	17.1	23.6	0.5	3.1131
221805_at	AW469184	major histocompatibility complex, class I, B	2.2	0.5	5.4	5.2	5.8	5.2	3.4	7.6	5.1	14.8	12.0	24.6	19.2	2.0	2.4	2.1	5.2	1.5	1.8	3.11
37384_at	D13640	retinitis pigmentosa GTPase regulator interacting protein 1 (RPGRIP1)	2.5	3.0	3.4	3.8	3.8	6.7	6.6	7.6	6.8	25.2	17.9	21.3	29.4	2.6	2.5	2.5	7.4	1.8	2.8	3.0985
206608_s_at	NM_020366.1	Toll-like receptor 2	1.1	1.4	1.2	0.8	1.0	1.1	1.0	0.5	1.4	6.1	3.4	5.3	4.7	1.5	0.9	0.8	1.3	0.5	0.7	3.091
204924_at	NM_003264.1	CD95, Fas, APO-1	1.6	0.1	2.1	8.2	7.6	2.8	0.4	0.8	1.4	52.9	88.0	94.4	99.8	1.6	1.3	0.1	26.3	0.9	0.4	3.0909
204781_s_at	NM_000043.1	KIAA0993	2.0	1.1	5.9	11.0	8.9	5.4	4.4	6.8	7.0	20.6	27.1	27.0	29.1	0.3	5.2	5.3	4.0	2.0	3.8	3.0827
212606_at	A1806395	FLAME-1	2.0	2.0	0.0	0.7	0.6	0.7	0.0	0.1	0.1	19.0	14.3	25.0	26.9	0.1	0.2	0.3	6.6	0.0	3.4	3.0797
211316_x_at	AF009616.1	ninjurin 1	3.1	2.9	20.1	19.4	31.9	11.6	11.9	20.8	19.1	59.8	74.1	72.8	81.0	4.1	6.8	8.7	10.3	5.5	2.6	3.0752
203045_at	NM_004148.1	intercellular adhesion molecule 3 (ICAM3)	4.4	2.5	3.2	6.4	4.8	10.7	9.7	18.5	12.1	29.3	34.1	44.7	46.1	0.5	1.2	1.7	8.3	0.2	2.9	3.0746
204949_at	NM_002162.2	carbonic anhydrase IV (CA4)	3.0	3.7	5.7	46.3	34.5	38.9	51.6	94.5	93.7	161.1	168.3	239.1	241.1	4.5	13.6	21.0	17.6	19.9	1.3	3.0617
206208_at	NM_000717.2	metallophosphoesterase	0.2	0.6	0.1	0.1	0.1	1.1	0.7	1.0	0.8	5.6	5.2	2.8	2.4	1.2	0.1	0.1	0.1	0.1	0.1	3.0572
213727_x_at	A1743654	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog (LYN)	2.1	1.7	5.0	15.0	12.1	8.9	13.7	25.4	23.9	49.9	28.3	59.9	75.8	0.7	4.5	6.6	5.7	5.4	3.7	3.0554
202626_s_at	NM_002350.1	immunoglobulin superfamily, member 6 (IGSF6)	15.5	9.5	12.1	12.7	14.8	32.6	31.6	54.0	41.0	110.1	115.1	122.7	127.2	18.4	2.1	1.5	38.8	33.0	0.6	3.0541
206420_at	NM_005849.1	protein kinase C and casein kinase substrate in neurons 2 (PACSN2)	1.1	0.3	0.2	0.4	0.7	1.9	1.2	1.1	1.0	17.5	24.2	30.6	33.3	1.4	0.4	0.4	8.4	0.3	0.3	3.0442
201651_s_at	NM_007229.1	zinc finger protein 267	21.4	17.4	4.6	24.8	20.1	13.3	19.5	33.9	35.3	61.3	72.5	76.1	94.4	24.7	4.9	4.4	8.6	6.1	8.0	3.0391
219540_at	AU150728	v-raf-1 murine leukemia viral oncogene homolog 1 (RAF1)	2.0	1.0	1.3	3.7	3.6	2.0	1.5	4.4	3.7	6.7	6.9	9.2	9.9	1.0	2.1	1.3	1.0	1.6	0.1	3.0361
201244_s_at	NM_002880.1	mitogen-activated protein kinase kinase 4	6.0	5.4	12.4	32.8	33.1	14.9	19.0	27.3	25.7	60.4	58.2	89.2	86.2	2.2	6.6	11.3	12.8	7.8	7.3	3.0329
203265_s_at	AA810268	IAR receptor-like protein-tyrosine phosphatase	1.4	1.2	2.8	6.4	4.5	1.7	2.6	3.5	3.1	12.8	12.8	10.4	16.8	1.4	1.4	1.3	1.3	2.5	1.5	3.028
203030_s_at	AF007555.1	zinc finger protein 217	0.0	0.0	1.6	1.2	0.1	0.1	0.1	0.1	0.1	0.8	3.0	1.1	2.8	0.1	0.1	0.0	0.1	0.0	0.0	3.0269
203739_at	NM_006526.1	interferon-induced protein with tetrahydropeptide repeats 4 (IFIT4)	1.9	2.6	3.0	18.4	8.4	7.6	8.0	14.7	14.9	37.3	45.1	24.4	27.0	1.2	4.6	5.3	6.1	5.5	3.6	3.0158
204747_at	NM_001549.1	carbonic anhydrase IV (CA4)	2.0	3.0	4.9	6.0	3.5	4.3	12.4	4.4	3.0	24.2	27.0	15.4	12.0	0.3	1.8	1.2	8.2	1.4	2.6	3.0143
206209_s_at	NM_000717.2		0.7	1.0	0.8	0.6	0.6	2.2	2.1	1.5	2.1	13.8	7.4	4.7	3.5	2.1	1.0	0.5	0.9	1.0	0.5	3.0112

## D. Mast cell (MC)-selective transcripts (1/2).

Probe set	Accession #	Transcripts	MC cord blood	MC lung	Ba 1	Ba 2 (small)	Ba 3 (small)	Eo 1	Eo 2	Eo 3 (small)	Eo 4 (small)	Ne 1	Ne 2	Ne 3 (small)	Ne 4 (small)	pl	CD4	CD8	CD14	CD19	Fb	MC.S.I.
217023_x_at	AF099143	tryptase beta	169.4	118.7	0.7	1.1	0.4	0.1	0.1	0.5	0.1	0.1	0.2	0.1	0.6	0.4	0.3	0.1	0.2	0.1	0.2	202.148
215382_x_at	AF206666.1	tryptase beta	168.1	108.4	1.7	0.7	0.4	0.2	0.2	0.2	0.1	0.1	0.3	0.1	0.1	0.1	0.7	0.1	0.1	0.1	0.5	172.668
204041_at	NM_000898.1	monoamine oxidase B	23.5	46.9	0.2	0.7	0.1	0.1	0.2	0.6	0.3	0.3	0.1	0.2	0.1	0.2	0.1	0.2	0.1	0.2	0.1	136.311
210084_x_at	AF206665.1	tryptase alpha	131.1	92.3	0.7	1.2	1.2	0.2	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.6	0.1	0.0	0.1	0.1	0.1	112.376
216474_x_at	AF206667.1	tryptase beta	210.0	120.9	2.4	2.0	1.4	1.2	0.4	0.2	0.1	0.2	1.1	0.1	0.1	1.8	0.8	0.9	0.9	0.1	0.1	84.3375
205683_x_at	NM_003294.2	tryptase beta	195.5	95.3	2.4	2.7	0.3	0.2	0.2	0.6	0.6	0.4	0.1	0.4	1.0	2.0	0.7	0.2	0.3	0.2	0.1	67.2617
207741_x_at	NM_003293.2	tryptase alpha	175.0	99.7	2.2	2.2	1.8	0.5	0.2	0.3	0.2	0.6	0.2	0.3	0.3	2.2	0.7	0.1	0.5	0.3	0.6	59.015
207134_x_at	NM_024164.2	tryptase beta	214.6	112.3	3.1	3.8	1.7	1.2	0.3	0.8	0.6	0.3	0.8	0.4	0.1	0.5	0.2	0.1	1.1	0.4	0.2	57.1834
205653_at	NM_001911.1	cathepsin G	91.2	57.0	2.7	1.1	0.9	0.9	0.4	3.1	0.8	0.3	1.4	1.6	0.6	0.7	0.2	0.4	1.3	0.3	0.2	51.4749
205266_at	NM_002309.2	leukemia inhibitory factor	17.0	9.8	0.2	0.2	0.3	0.3	0.1	0.2	0.2	0.1	0.2	0.1	0.4	0.7	0.1	0.2	0.1	0.1	0.1	44.3659
210324_at	M17263.1	complement protein C8 gamma	2.9	6.9	0.1	0.1	0.0	0.0	0.0	0.1	0.1	0.3	0.1	0.1	0.1	0.1	0.1	0.0	0.0	0.0	0.1	33.806
211743_s_at	BC005929.1	major basic protein	74.3	70.7	1.0	4.7	2.7	0.1	0.7	0.8	0.6	0.2	0.3	0.7	0.2	0.1	0.2	0.2	0.3	0.2	0.3	31.5959
211549_s_at	U63296.1	15-hydroxyprostaglandin	48.3	48.3	2.1	2.5	1.4	1.5	1.3	0.8	0.9	0.1	0.1	0.2	0.1	1.1	0.5	0.8	0.5	0.5	0.0	24.8454
206726_at	NM_014485.1	prostaglandin D2 synthase	119.0	94.0	5.0	7.8	5.7	0.7	0.1	1.0	0.5	0.2	0.2	0.2	0.6	1.3	0.7	0.3	1.2	0.3	0.0	17.432
205011_at	NM_014622.1	loss of heterozygosity, 11,	76.1	70.9	3.0	6.8	4.5	2.3	1.0	1.4	1.9	0.2	1.1	1.2	1.8	2.9	2.2	1.3	1.7	2.0	2.6	16.2511
205428_s_at	NM_001740.2	chromosomal region 2, gene A	16.7	63.4	1.3	0.7	0.9	0.4	1.6	0.7	1.3	1.8	1.6	3.6	1.5	1.7	0.7	1.1	1.3	0.6	0.9	16.1621
219225_at	NM_024554.1	calbindin 2	10.0	9.2	0.1	0.1	0.1	0.2	0.1	0.6	0.6	0.1	0.6	0.1	0.2	0.1	0.6	0.1	0.6	0.0	0.2	15.639
204488_s_at	NM_005424.1	FLJ11413	3.6	2.8	0.5	0.3	0.1	0.0	0.1	0.2	0.0	0.0	0.0	0.1	0.1	0.0	0.0	0.0	0.1	0.0	0.0	14.4259
208343_s_at	AF148343.1	lysine kinase with immunoglobulin and epidermal growth factor homology domains	1.5	0.9	0.0	0.0	0.3	0.1	0.0	0.1	0.0	0.1	0.0	0.2	0.4	0.1	0.0	0.0	0.0	0.0	0.0	13.8025
205051_s_at	NM_000222.1	CYP1A promoter binding factor	92.1	85.8	6.2	8.1	7.3	2.3	5.2	8.5	2.7	0.7	2.1	0.8	1.1	0.8	0.2	0.5	0.1	0.1	0.5	12.3815
210102_at	BC001234.1	CD117 c-KIT	40.9	41.1	2.8	3.7	4.5	0.3	0.4	0.3	0.6	0.7	0.9	0.2	0.6	1.8	0.8	0.7	1.2	0.6	1.3	11.3619
210796_x_at	D86359.1	loss of heterozygosity, 11,	17.8	26.0	1.5	1.0	1.1	1.2	1.5	1.3	1.4	1.4	2.3	1.7	1.3	2.0	1.4	1.5	1.8	1.0	0.8	10.5398
206519_x_at	D86358.1	chromosomal region 2, gene A	3.4	7.9	0.0	0.3	0.4	0.0	0.0	0.0	0.1	0.0	0.1	0.5	0.2	0.5	0.0	0.0	0.0	0.4	0.0	10.13
206480_at	NM_000897.1	sialic acid binding Ig-like lectin, siglec6	8.8	16.0	0.3	0.2	0.6	2.4	1.6	0.5	0.1	0.2	1.1	0.1	0.1	1.3	0.1	0.3	0.1	0.1	0.4	9.27381
206617_s_at	NM_002910.4	leukotriene C4 synthase	10.6	6.2	1.2	0.1	0.4	2.8	1.6	0.5	0.1	0.6	2.1	0.1	0.1	0.9	0.2	0.7	0.3	0.4	0.1	9.18529
208089_s_at	NM_030784.1	renin-binding protein	6.0	13.4	0.8	0.6	0.2	0.5	0.7	0.5	0.5	0.1	0.6	0.3	0.0	0.7	0.7	1.1	0.8	0.6	1.0	8.10897
205466_s_at	NM_005114.1	tudor domain containing 3	18.1	7.2	0.1	0.4	0.1	0.7	0.1	0.3	0.2	0.4	0.1	0.8	0.4	0.1	0.0	0.0	0.2	1.4	—	8.15381
214913_at	AB002364.1	heparan sulfate 3-O-sulfotransferase	6.8	4.3	0.5	0.7	0.8	0.5	0.7	0.6	0.4	0.5	0.4	0.7	1.2	0.7	0.6	0.5	0.4	0.5	0.5	7.2214
201860_s_at	NM_000930.1	ADAMTS3 a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 3	22.2	29.7	0.2	0.4	0.1	0.1	0.3	0.5	0.5	0.1	0.1	1.3	0.4	1.6	0.1	0.2	0.6	0.1	3.6	7.10135
206520_x_at	NM_001245.1	tissue-plasminogen activator	19.0	22.7	2.4	1.1	0.8	1.1	1.5	1.3	1.0	2.0	2.0	0.4	1.4	2.9	2.1	2.3	1.9	1.9	1.2	7.10132
220532_s_at	NM_014020.1	sialic acid binding Ig-like lectin, siglec6	52.4	18.2	0.8	0.8	1.0	6.4	2.9	1.5	1.2	0.4	0.3	1.4	0.6	2.2	0.6	0.2	5.0	0.1	0.0	6.1662
218169_at	NM_018052.1	LR8 protein	6.2	14.6	0.3	0.2	0.4	0.4	0.3	0.3	0.4	0.6	0.5	0.1	0.5	0.5	0.2	1.4	1.6	0.3	1.0	6.04597
221728_x_at	AK025198.1	FLJ10305	5.6	5.5	0.6	0.9	1.0	0.4	3.6	0.9	0.8	0.7	0.6	1.4	0.9	0.9	0.8	0.7	0.7	0.8	0.5	5.70228
214028_x_at	AU156998	nuclear receptor subfamily 1, group 1, member 3	3.2	11.9	0.9	0.0	0.4	0.8	0.3	0.4	0.7	0.6	0.6	0.1	0.1	0.8	1.2	1.1	0.1	0.7	0.9	5.10738
221552_at	BC001698.1	tudor domain containing 3	10.6	3.4	0.9	1.8	1.1	0.9	1.1	1.0	0.9	0.2	0.2	0.7	0.1	0.1	0.2	0.7	0.9	0.3	1.1	5.02434
203367_at	NM_007026.1	lipase	15.0	45.4	1.2	0.9	0.8	0.9	0.9	0.8	0.1	0.2	0.7	0.4	2.0	0.9	1.0	2.7	0.5	1.4	5.2	5.00514
206997_s_at	NM_004807.1	MKP-1 like protein tyrosine phosphatase (MKP-L)	4.2	3.8	0.2	0.1	0.1	0.1	0.4	0.4	0.1	0.3	0.3	0.4	0.3	0.7	0.3	0.2	0.8	0.3	0.2	4.81127
		heparan sulfate 6-O-sulfotransferase																				

## D. Mast cell (MC)-selective transcripts (2/2).

Probe set	Accession #	Transcripts	MC, cord blood	MC, lung	Ba 1	Ba 2 (small)	Ba 3 (small)	Eo 1	Eo 2	Eo 3 (small)	Eo 4 (small)	Ne 1	Ne 2	Ne 3 (small)	Ne 4 (small)	pl	CD4	CD8	CD14	CD19	Fb	MC S.I.
207480_s_at	NM_020149.1	TAL1 homeobox protein Meis2e	14.0	14.9	1.9	3.6	4.0	1.7	1.9	5.3	3.8	0.3	0.6	1.0	0.3	0.5	0.8	0.4	0.6	0.4	0.8	4.72642
45288_at	AA209239	lipase	10.9	3.0	0.2	2.1	0.8	0.5	0.5	1.3	0.9	0.1	0.1	0.2	0.1	0.4	0.5	0.5	1.3	1.0	0.9	4.52869
207039_at	NM_000077.1	cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4)	7.5	3.6	0.7	0.7	0.1	0.6	0.4	0.3	0.5	0.1	1.2	0.6	1.1	0.1	0.9	0.5	0.8	0.1	1.2	4.35629
201650_at	NM_002276.1	keratin 19	6.2	12.0	0.0	0.0	0.3	0.1	0.0	0.0	0.0	0.0	0.1	0.1	0.1	0.1	0.0	0.1	0.1	0.0	2.0	4.35647
214533_at	NM_001836.1	chymase	10.1	2.7	0.4	0.2	0.8	0.1	0.1	0.8	0.6	0.1	0.1	0.2	0.2	1.2	0.7	0.5	1.0	0.4	0.3	4.27984
218211_s_at	NM_024101.1	melanophilin	24.8	29.6	2.7	2.5	1.8	3.0	2.5	1.9	2.2	4.6	4.1	3.3	4.1	6.4	4.0	3.2	2.4	3.4	2.7	4.24499
203916_at	NM_003635.1	N-deacetylaseN-sulfotransferase erythrocyte membrane protein band 4.1-like 1	17.9	26.7	3.2	6.5	6.8	2.5	2.7	3.6	3.1	4.2	3.4	5.5	5.2	0.9	3.1	4.9	3.3	2.7	2.4	4.20693
212336_at	AB022336.1	calhopsin D	3.8	6.4	0.1	0.2	0.1	0.5	0.1	0.2	0.4	0.1	0.1	0.1	0.5	0.1	0.4	0.2	0.4	0.4	1.2	4.12758
200766_at	NM_001909.1	delta-6 fatty acid desaturase (FADS6)	42.6	39.5	2.5	5.3	4.3	4.3	4.8	3.4	2.7	4.0	6.7	3.1	1.9	2.6	1.6	2.5	10.0	1.8	5.9	4.1037
202218_s_at	NM_004265.1	centaurin, gamma 2	18.8	24.5	0.4	0.2	1.0	0.3	0.1	0.8	0.5	0.2	0.1	0.1	0.1	1.6	0.1	0.6	0.1	0.6	5.3	4.08548
204066_s_at	NM_014914.1	cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4)	5.3	7.9	0.4	0.4	0.7	0.2	0.2	0.6	0.6	0.3	0.5	0.4	0.4	0.8	0.6	1.8	0.6	1.0	1.6	4.06712
205644_x_at	U36945.1	lipase	14.0	6.4	1.0	1.4	0.7	1.2	1.3	1.7	1.5	1.0	1.6	1.5	2.1	2.3	1.8	1.5	0.9	0.3	2.4	3.88459
221679_s_at	AF225418.1	heat shock protein 70kD	2.8	1.9	0.4	0.9	0.1	0.3	0.4	0.4	0.1	0.1	0.5	0.0	0.5	0.5	0.1	0.6	0.6	0.5	0.2	3.83039
211538_s_at	U56725.1	15-hydroxyprostaglandin dehydrogenase member 2	4.4	7.4	0.3	0.6	0.4	0.6	0.3	0.3	0.9	1.4	0.4	1.0	0.8	1.5	0.5	0.5	0.1	0.5	0.7	3.80423
211548_s_at	J05594.1	nuclear receptor subfamily 5, group A, member 2	82.6	60.0	19.4	26.0	16.3	3.2	2.9	1.8	1.7	0.8	0.5	0.9	0.2	4.1	1.2	0.9	0.1	0.6	0.2	3.49258
210174_at	AF228413.1	RAB38, member RAS oncogene	2.9	3.4	0.5	0.5	0.6	0.8	1.1	0.7	1.2	1.1	0.4	0.1	0.4	0.9	0.7	0.2	0.2	0.6	0.3	3.47124
219412_at	NM_022337.1	gelosin-like capping protein (actin filament)	3.9	4.0	0.1	0.4	0.3	0.7	0.1	0.2	0.3	0.2	0.2	1.1	0.1	1.2	0.1	0.8	0.4	0.1	0.5	3.32805
201850_at	NM_001747.1	KIAA0555	70.5	64.5	9.6	30.8	28.8	8.1	7.8	11.5	9.9	2.6	3.6	3.0	2.4	1.6	1.1	1.0	17.0	5.8	5.3	3.29919
205888_s_at	A1962693	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1	5.4	4.6	0.7	1.6	1.2	0.8	0.7	0.1	1.0	1.3	0.3	0.2	0.6	1.2	0.3	1.5	0.7	1.2	0.4	3.25197
221750_at	BG035985	nuclear receptor subfamily 1, group 1, member 3	5.0	3.6	0.9	1.5	1.1	1.1	1.2	1.3	1.0	1.3	0.5	0.7	1.2	0.7	0.5	1.1	0.7	1.4	1.2	3.1928
214218_s_at	AV699347	FLJ21080	3.5	3.5	0.7	0.6	0.7	0.5	2.2	0.5	0.5	0.7	1.2	0.6	0.1	1.1	0.9	0.3	0.6	0.8	0.4	3.15254
218788_s_at	NM_022743.1	SH3-domain protein 5 (ponsin)	16.1	23.7	0.5	2.3	2.5	0.9	1.1	2.7	2.1	1.1	1.0	0.8	0.9	2.3	2.1	2.9	0.6	2.0	6.3	3.07851
218087_s_at	NM_015385.1	prostate differentiation factor	1.4	1.9	0.4	0.9	0.4	0.5	0.0	0.0	0.1	0.0	0.1	0.1	0.2	0.1	0.0	0.2	0.2	0.2	0.1	3.07366
221577_x_at	AF003934.1	GM2 activator protein	7.8	5.5	0.6	0.3	0.5	0.6	0.1	0.2	0.6	0.0	0.2	0.3	0.1	0.1	0.2	0.0	0.1	0.4	2.1	3.05532
35820_at	X62078	heat shock 105kD	21.8	17.6	1.4	3.3	1.3	0.3	0.3	0.2	0.5	0.5	0.8	1.9	0.3	0.4	0.2	0.2	6.5	5.0	2.7	3.01647
206744_x_at	BG403660		7.3	4.8	0.5	0.2	0.2	0.9	0.1	0.4	0.6	0.1	0.1	0.3	0.1	0.8	1.7	2.0	0.9	0.9	2.0	3.00571

## E. Basophil and eosinophil-selective transcripts (1/1).

Probe set	Accession #	Transcripts	MC, cord blood	MC, lung	Ba 1	Ba 2	Ba 3	EO 1	EO 2	EO 3	EO 4	Ne 1	Ne 2	Ne 3 (small)	Ne 4 (small)	pI	CD 4	CD 8	CD 14	CD 19	Fb	Ba+EO S.I.
211517_s_at	M96651.1	IL-5R interleukin 5 receptor alpha	0.6	0.1	11.8	28.2	17.9	16.4	25.3	32.6	29.5	0.0	0.7	0.0	1.0	0.0	0.4	0.2	0.0	0.2	0.0	61.956
210744_s_at	M75914.1	IL-5R interleukin 5 receptor alpha CRTH2 chemotactant	0.2	1.6	15.4	30.8	15.3	18.7	40.2	29.7	33.0	0.3	0.2	1.5	0.5	0.1	0.1	0.1	0.1	0.2	0.1	42.811
206361_at	NM_004778.1	receptor-homologous molecule expressed on Th2 cells	1.8	0.3	22.0	40.5	15.3	33.7	37.9	38.9	42.3	1.0	2.6	2.2	2.1	0.8	1.4	1.0	1.2	0.9	0.5	16.642
206207_at	NM_001828.3	Charcot-Leyden crystal protein	1.1	0.1	270.0	219.1	203.6	226.8	233.8	179.7	163.1	2.1	19.4	19.1	49.3	2.8	1.0	1.4	0.9	0.7	0.4	15.164
203638_s_at	NM_022969.1	fibroblast growth factor R 2 egf-like module containing, mucin-like, hormone receptor-like sequence 1 (EMR-1)	0.2	0.1	7.3	43.5	33.0	4.1	8.8	12.3	23.3	0.1	0.1	0.3	0.3	0.1	0.1	0.2	0.1	0.1	1.0	13.357
207111_at	NM_001974.1	FLJ11581 fls, clone HEMBA1003598 dachshund (Drosophila) homolog	1.5	0.1	16.4	49.5	34.5	85.9	93.1	91.2	93.5	2.7	3.7	5.4	5.1	3.4	1.7	0.8	7.1	1.8	0.5	8.0092
215248_at	AU145003	Hs.63931	0.7	0.3	5.7	4.7	5.2	4.5	2.1	2.8	2.1	1.0	0.1	0.1	0.1	0.2	0.1	0.1	0.1	0.1	0.2	7.2618
205471_s_at	AW772082	FLJ22316	0.1	0.6	5.1	4.1	3.7	6.4	8.3	9.0	7.6	0.8	0.9	1.0	0.8	0.1	0.1	0.3	0.5	0.0	0.1	6.8198
218857_s_at	NM_025080.1	histamine receptor H4	1.0	7.0	18.0	35.3	18.6	13.7	12.5	16.3	15.4	1.3	1.7	0.9	1.9	0.3	0.5	0.4	2.4	0.2	0.2	6.5045
221169_s_at	NM_021824.1	entropin	0.2	0.5	4.5	12.5	8.9	1.9	2.6	4.2	2.9	0.5	0.6	1.1	0.6	0.4	0.7	0.5	0.7	0.0	0.3	5.9783
201769_at	NM_014666.1	secreted fibroblast growth factor receptor (K-sam-III)	7.8	9.1	41.7	101.5	76.0	26.8	34.1	40.5	35.7	3.0	2.9	3.6	4.2	4.5	6.3	6.9	8.0	9.0	7.9	5.1015
208228_s_at	M87771.1	hypothetical protein LOC283445	0.3	1.4	3.7	10.2	8.3	3.9	8.9	4.5	8.3	0.8	1.4	1.1	0.5	1.3	0.4	0.7	0.3	0.5	1.1	4.9922
213605_s_at	AL049987.1	CD244 natural killer cell receptor 2B4	0.8	0.0	10.8	46.8	44.7	6.7	6.1	25.8	20.6	1.3	1.4	4.5	4.2	2.9	1.1	2.1	3.7	2.0	0.3	4.7426
205382_s_at	NM_001928.1	edisin	3.5	0.1	62.0	206.0	176.5	62.4	48.1	60.5	44.8	7.1	32.5	20.5	16.3	0.1	0.6	0.1	15.6	0.1	3.8	4.7202
49452_at	A1057637	hypothetical protein LOC283445	0.6	0.2	5.2	7.7	8.6	6.9	5.9	10.2	12.7	1.1	0.2	0.3	1.3	0.1	1.6	1.6	0.5	1.3	0.8	4.7183
220307_at	NM_016382.1	calcium channel, voltage-dependent, L type, alpha 1D subunit	0.5	0.1	15.7	87.0	65.4	9.9	10.8	26.8	18.5	0.3	0.4	1.2	3.0	0.1	0.4	3.5	5.2	1.1	0.1	4.6297
210108_at	BE550599	protein kinase-related oncogene (PIM1)	0.2	0.1	1.0	1.7	2.4	0.9	0.8	2.4	1.8	0.0	0.6	0.5	0.5	0.0	0.3	0.1	0.0	0.3	0.0	4.5958
209193_at	M24779.1	inositol	8.8	7.1	61.3	110.3	100.1	47.0	79.7	91.8	78.5	19.2	18.8	21.1	16.1	4.1	12.7	13.9	4.8	4.0	1.2	4.1983
202794_at	NM_002194.2	polyphosphate-1-phosphatase (INPP1)	5.7	6.2	7.1	25.8	20.5	17.9	24.8	53.6	57.8	2.8	2.7	2.6	4.0	1.9	1.8	2.8	4.8	1.9	4.8	4.1158
208304_at	NM_001837.1	CCR3 chemokine (C-C motif) receptor 3	0.2	1.1	107.2	142.9	102.2	46.4	91.7	118.1	107.5	28.3	20.0	26.3	25.1	0.2	0.5	0.4	0.2	0.2	0.4	3.9525
206111_at	NM_002934.1	eosinophil-derived neurotoxin	2.2	2.0	33.7	71.4	38.4	104.7	80.8	47.7	45.1	2.0	2.3	3.1	2.8	1.4	0.7	0.4	14.8	0.7	0.5	3.7641
43427_at	A1970898	hypothetical protein LOC283445	0.8	0.7	2.1	4.8	4.3	5.1	4.6	8.0	6.4	1.0	0.8	0.7	0.8	1.1	1.0	1.3	0.6	1.1	1.1	3.7554
213804_at	A1039084	inositol	0.6	1.2	4.3	8.0	6.8	8.6	5.6	6.3	9.7	0.7	0.5	2.2	1.7	1.4	1.2	1.4	1.0	1.9	1.3	3.6088
209906_at	U62027.1	C3a receptor	12.4	11.2	44.1	72.3	50.5	18.8	38.8	70.3	29.9	1.2	1.2	1.8	3.8	1.6	1.6	1.5	3.0	0.6	0.5	3.6039
202804_at	A1539710	ATP-binding cassette, sub-family C (CFTR/MRP), member 1	8.5	7.0	24.2	56.2	48.9	14.2	20.0	30.1	20.7	3.0	3.6	4.3	6.0	3.8	3.5	5.4	5.1	5.5	5.3	3.5673
221675_s_at	AF195624.1	cholinephosphotransferase 1 beta	7.0	6.8	31.6	79.7	55.8	26.9	32.6	43.8	41.8	5.2	7.5	5.9	9.6	2.4	3.1	3.3	7.7	11.8	5.7	3.5626
201582_s_at	NM_003104.1	sorbinol dehydrogenase (SORD)	2.0	1.5	2.9	4.2	4.1	7.4	11.6	8.3	11.2	1.7	2.5	1.5	1.3	1.3	1.4	1.8	1.2	1.8	1.1	3.5098
210230_at	BC003629.1	FLJ23438 fls, done HRC13275	1.7	0.1	8.3	11.0	13.3	2.4	5.1	5.1	4.1	0.1	0.5	0.2	0.7	0.3	0.2	0.6	0.8	1.9	0.5	3.2532
219919_s_at	NM_018276.1	FLJ10928	0.1	0.2	3.1	1.8	2.5	1.7	4.3	1.7	2.1	0.1	0.5	0.4	0.3	0.1	0.1	0.1	0.1	0.1	0.7	3.2497
204301_at	NM_014867.1	KIAA0711	0.6	0.1	3.8	14.3	10.7	5.3	6.8	12.6	10.5	1.2	0.6	1.6	1.6	1.0	0.8	1.2	2.6	0.8	0.1	3.2398
210999_s_at	U66065.1	Gri10- and Gri1-IR-related splice variant 1	3.6	1.7	8.4	13.6	11.8	7.3	4.6	4.8	6.4	2.2	1.7	1.9	2.0	1.9	1.2	1.2	1.6	0.4	1.6	3.1044
209539_at	D25304.1	RacCdc42 guanine exchange factor (GEF) 6	13.1	24.8	28.8	74.7	73.0	53.8	35.5	92.9	59.6	9.2	6.1	18.5	13.7	3.1	10.8	12.9	7.1	7.8	1.0	3.0943
208921_s_at	L12387.1	sorcin (SRI)	19.2	11.4	20.2	88.6	67.0	37.4	42.4	86.3	85.4	6.9	8.9	17.6	21.5	2.6	11.1	12.7	8.4	8.6	17.8	3.0628
209043_at	AF03026.1	trifunctional ATP sulfurylaseadenosine 5-phosphosulfate kinase	19.9	16.1	39.0	87.1	75.2	66.4	68.7	89.4	71.4	13.8	20.0	46.5	8.9	6.3	8.7	4.4	10.6	11.0	22.7	3.0385

## F. Eosinophil and neutrophil-selective transcripts (1/1).

Probe set	Accession #	Transcripts	MC cord blood	MC lung	Ba 1	Ba 2 (small)	Ba 3 (small)	EO 1	EO 2	EO 3 (small)	EO 4 (small)	Ne 1	Ne 2	Ne 3 (small)	Ne 4 (small)	pl	CD4	CD8	CD14	CD19	Fb	EO+Ne S.I.
221345_at	NM_005306.1	GPR	0.1	0.4	0.9	0.6	0.6	7.0	18.6	15.4	10.5	49.7	45.7	22.5	23.0	0.8	0.1	0.1	0.7	0.4	0.1	21.742
212860_at	BG168720	GPR43, PAR1-like zinc finger, D1HC domain containing 18	2.2	0.8	4.1	3.9	4.0	16.0	17.4	14.8	16.7	59.2	53.9	30.9	39.8	1.1	2.4	3.8	2.6	1.5	1.3	6.5842
211576_s_at	BC003068.1	solute carrier family 19 member 1	1.4	0.1	0.7	1.4	0.7	5.1	5.9	11.5	12.4	19.8	18.7	27.1	28.1	1.8	0.9	0.4	2.7	0.5	0.8	4.99
214321_at	BF440025	nephroblastoma overexpressed gene ARF-GAP, RHO-GAP, ankyrin repeat and pleckstrin homology domains-containing protein 3	1.3	1.0	0.8	0.2	0.7	6.2	7.2	17.0	13.7	4.5	7.6	10.7	11.3	0.1	0.1	0.0	0.1	0.1	1.8	4.9823
218950_at	NM_022481.1	BCL2-related protein A1	1.4	3.1	2.4	3.7	2.1	15.5	15.9	18.3	15.5	28.0	24.3	15.9	20.6	0.7	0.2	0.8	3.9	0.9	1.0	4.829
205681_at	NM_004049.1	granulysin	0.5	1.9	1.0	3.2	2.4	52.4	40.2	35.9	30.5	46.5	49.2	35.5	33.5	1.5	2.2	1.9	8.3	4.3	0.2	4.7782
203785_at	NM_012198.1	cDNA FLJ36416 fis, clone THYMU2011053	2.0	1.8	4.5	11.7	8.3	27.5	39.8	46.7	34.8	71.6	85.2	80.5	77.9	1.0	1.0	1.2	12.1	3.1	0.5	4.4403
213241_at	AF035307.1	hypothetical protein PRO2631	5.0	2.4	1.6	1.0	1.0	33.2	37.1	68.7	40.6	63.2	77.8	89.2	80.9	3.0	3.0	2.8	13.5	4.1	7.8	4.2603
221815_at	BE671816	homolog of yeast long chain polyunsaturated fatty acid elongation enzyme 2	1.2	1.4	1.3	0.5	1.6	10.1	8.8	11.2	6.4	5.0	6.2	4.0	3.8	1.6	0.8	0.2	1.4	0.9	0.6	4.1325
214153_at	BE467941	KIAA0599	1.0	0.6	1.0	2.0	3.1	9.1	10.4	18.2	16.6	9.7	9.7	14.5	15.2	0.8	0.9	1.2	0.7	2.3	0.1	4.0787
212821_at	AU147160	Edg4, endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 4	0.1	0.1	0.4	1.2	0.9	4.6	2.8	4.7	3.4	4.4	3.5	6.0	7.9	0.4	0.2	0.4	0.3	0.0	0.2	3.727
206723_s_at	AF011466.1	adenosine monophosphate deaminase 2 (isoform L)	1.2	1.4	2.1	3.6	2.6	13.7	8.0	19.6	22.3	24.6	17.0	26.1	29.1	0.1	3.6	5.0	3.8	1.9	0.9	3.7119
212360_at	A1916249	transforming, acidic coiled-coil containing protein 3 (TACC3)	1.0	2.0	2.8	5.9	4.8	26.6	18.7	30.2	31.9	78.7	63.1	79.5	91.3	3.4	5.8	6.1	12.8	3.7	5.8	3.5888
218308_at	NM_006342.1	protein kinase C-like 2	0.4	0.4	4.8	8.3	9.5	3.3	2.4	3.3	4.7	17.6	14.8	23.5	22.8	2.4	2.3	1.8	3.6	1.0	0.7	3.4769
212629_s_at	AK023692.1	serumglucocorticoid regulated kinase (SGK)	1.9	0.6	3.1	3.7	5.1	11.8	7.6	17.7	13.8	16.7	23.6	27.0	28.4	1.1	2.1	2.2	4.2	4.2	2.9	3.2963
201739_at	NM_005627.1	ectonucleoside triphosphate diphosphohydrolase 1	30.2	25.2	1.9	18.5	25.4	114.1	118.0	150.9	164.8	60.2	77.1	105.8	156.3	1.1	3.7	0.7	34.6	1.8	18.9	3.2458
209473_at	AV717590	growth arrest and DNA damage inducible protein beta (GADD45B)	1.4	0.8	2.1	1.6	2.0	15.9	22.3	39.5	29.1	14.1	13.7	23.7	13.8	2.6	2.6	1.3	6.5	4.8	0.6	3.0752
209304_x_at	AF087853.1	iduronate 2-sulfatase	2.0	0.3	2.7	4.5	3.6	15.5	11.9	16.3	34.4	7.0	12.0	13.5	9.4	0.4	3.1	4.2	4.1	3.7	0.6	3.0295
210686_at	AF050145.1		0.1	0.3	1.3	0.5	1.7	7.1	2.9	3.3	3.8	6.1	5.1	5.2	10.8	0.4	0.1	0.9	0.7	0.4	0.1	3.0005

## G. Basophil and neutrophil-selective transcripts (1/1)

Probe set	Accession #	Transcripts	MC, cord blood	MC, lung	Ba 1	Ba 2 (small)	Ba 3 (small)	Eo 1	Eo 2 (small)	Eo 3 (small)	Eo 4 (small)	Ne 1	Ne 2	Ne 3 (small)	Ne 4 (small)	pl	CD4	CD8	CD14	CD19	Fb	Ba+Ne S.I.
218739_at	NM_016006.1	CGI-58 protein	1.8	1.8	7.2	16.3	17.3	2.6	3.3	3.2	2.5	20.7	23.6	21.4	19.3	1.3	1.2	0.7	2.9	0.7	1.5	5.81398
219242_at	NM_025180.1	FLJ13386	1.0	0.3	10.1	23.5	18.8	2.4	3.7	4.5	4.2	13.7	14.0	26.1	27.7	0.1	0.5	1.6	1.0	0.6	2.5	4.97025
219157_at	NM_007246.1	kelch (Drosophila)-like 2	2.4	1.7	4.2	16.2	19.2	3.6	2.5	4.3	3.8	15.5	24.4	24.5	22.5	0.7	2.0	1.5	3.0	2.2	1.7	4.61523
206643_at	NM_002108.2	histidine ammonia-lyase	0.1	1.4	8.5	13.7	25.4	0.2	0.6	1.3	0.6	31.4	32.8	61.7	37.0	1.6	0.5	0.1	5.6	0.6	0.5	4.57355
213935_at	AF007132.1	clone 23551 mRNA	0.8	0.1	5.0	26.2	26.4	2.4	1.7	2.9	1.2	4.5	6.7	11.2	9.0	0.1	0.1	0.2	2.3	0.5	0.8	4.33664
222151_s_at	AK023738.1	FLJ13676 fis	1.0	0.9	4.5	5.5	4.7	1.8	1.7	1.4	1.6	8.4	10.2	8.4	7.6	0.5	0.8	1.3	0.8	1.0	1.3	4.14372
207907_at	NM_003807.1	tumor necrosis factor (ligand superfamily, member 14 (TNFSF14))	0.1	0.1	3.9	10.4	6.3	1.2	1.5	4.0	4.1	15.8	7.3	15.8	11.5	0.2	0.4	0.1	0.6	0.0	0.1	3.89177
202530_at	NM_001315.1	mitogen-activated protein kinase 14	5.0	3.0	28.8	82.2	70.8	4.0	7.1	13.9	11.1	13.6	23.0	25.7	22.3	5.3	2.9	3.5	7.3	2.6	4.5	3.8469
217571_at	N54942	Hs.276590 ESTs	0.1	0.1	5.5	18.9	20.9	0.3	0.3	1.6	0.7	19.6	14.5	29.9	18.4	0.4	0.8	0.9	4.3	1.0	0.3	3.84207
203693_s_at	NM_001949.2	E2F transcription factor 3	2.5	1.7	4.3	16.2	13.2	2.1	1.9	5.7	3.3	8.8	11.7	13.3	15.4	1.5	1.4	2.5	2.3	1.1	1.2	3.7116
203420_at	NM_016255.1	autosomal highly conserved protein (AHCPL)	2.4	3.3	15.6	31.5	32.4	7.3	6.6	14.3	11.0	37.2	37.2	48.5	50.0	6.1	5.0	9.8	4.5	3.3	9.8	3.48188
218308_at	NM_006342.1	transforming, acidic coiled-coil containing protein 3	0.4	0.4	4.8	8.3	9.5	3.3	2.4	3.3	4.7	17.6	14.8	23.5	22.8	2.4	2.3	1.6	3.6	1.0	0.7	3.4789
203080_s_at	NM_013450.1	bromodomain adjacent to zinc finger domain, 2B	2.2	2.4	10.4	22.8	22.9	4.9	6.6	10.0	9.5	29.5	30.7	33.5	40.6	1.1	1.7	1.9	4.6	2.3	1.5	3.401
219999_at	NM_018621.1	hypothetical protein PRO2198	0.4	0.6	3.9	7.6	8.0	2.0	1.5	3.9	2.7	9.8	6.5	11.7	12.3	0.2	1.3	1.8	2.4	1.7	0.9	3.31991
213805_at	A692428	clone 23551 mRNA	0.3	0.1	13.8	11.0	8.7	3.2	3.0	1.4	1.4	19.7	16.7	5.3	7.0	0.7	0.2	0.8	3.3	0.4	0.7	3.29317
204669_s_at	NM_007219.2	ring finger protein 24	0.9	0.2	4.4	27.9	34.3	2.1	5.9	16.1	14.5	18.8	14.4	60.7	56.1	0.5	0.1	0.1	0.1	0.1	0.1	3.18834
215555_at	AK023774.1	FLJ13712 fis	0.0	0.4	5.0	4.3	5.8	1.5	1.9	1.5	1.5	7.6	8.2	3.3	3.2	0.9	1.0	1.5	1.5	1.0	0.1	3.1591

## H. Mast cell and basophil-selective transcripts (1/1).

Probe set	Accession #	Transcripts	MC, cord blood	MC, lung	Ba 1	Ba 2 (small)	Ba 3 (small)	Eo 1	Eo 2	Eo 3 (small)	Eo 4 (small)	Ne 1	Ne 2	Ne 3 (small)	Ne 4 (small)	pl	CD4	CD8	CD14	CD19	Fb	MC+Ba S.I.
205624_at	NM_001870.1	carboxypeptidase A3	137.1	91.0	107.6	139.0	173.1	2.5	1.6	2.8	1.9	0.1	1.4	2.0	12.4	0.2	1.2	0.2	0.2	0.5	0.5	59.1989
208605_s_at	NM_002529.2	R TRK neurotrophin receptor regulator of G protein signaling (RGS13)	8.0	1.2	4.6	9.3	8.1	0.2	0.2	0.0	0.1	0.2	0.0	0.1	0.1	0.1	0.1	0.1	0.1	0.0	0.0	34.7309
210258_at	AF030107.1	R Fc epsilon R I beta	6.2	8.4	5.6	7.1	10.9	0.3	0.1	0.4	0.5	0.5	0.0	0.1	0.3	0.1	0.0	0.0	0.2	0.3	0.0	21.7762
207496_at	NM_000139.1	R Fc epsilon R I beta	19.9	24.7	35.4	51.9	45.6	0.9	0.1	0.5	0.3	0.1	0.1	0.5	1.8	1.6	0.5	0.2	0.0	0.3	0.1	21.1783
205857_at	AI269290	solute carrier family 18	24.3	27.1	8.1	22.3	25.0	1.3	1.0	0.8	0.9	1.3	0.9	0.5	0.7	0.9	0.4	0.3	0.2	0.3	0.3	20.3301
210358_x_at	BC002557.1	GATA-binding protein 2	18.4	12.8	55.0	31.7	24.7	2.0	1.6	1.9	1.7	0.9	1.9	1.3	3.7	2.6	0.8	0.8	0.9	0.4	2.7	9.46893
207497_s_at	D10583.1	Fc epsilon R I beta	10.7	28.6	34.9	12.6	6.8	1.5	1.0	0.8	0.8	1.9	0.9	1.7	1.5	1.7	0.7	0.7	0.1	0.3	0.5	9.39967
203914_x_at	NM_000860.1	15-hydroxyprostaglandin dehydrogenase (PDGH) chromosome 11 open reading frame 14	63.9	51.4	24.8	36.0	23.3	4.1	4.6	4.6	2.6	1.3	0.9	1.3	1.2	6.0	1.4	1.5	0.4	0.8	0.4	6.14285
219557_s_at	NM_020645.1	protein kinase, X-linked	7.4	4.2	4.4	7.4	6.6	1.2	1.6	2.0	2.4	0.9	1.9	1.1	2.1	1.1	1.4	1.4	1.5	0.4	1.6	3.38029
204061_at	NM_005044.1	low density lipoprotein receptor	6.2	5.2	5.2	12.8	16.9	2.3	2.7	2.5	2.4	0.8	0.4	0.7	1.2	1.9	1.5	2.1	2.5	2.0	0.8	3.26062
202088_s_at	NM_005272.2	R	24.6	16.8	19.3	28.5	13.5	1.6	1.0	1.6	0.9	0.8	2.4	1.5	2.5	2.3	2.1	3.4	3.5	0.8	6.3	3.1679

Figure 6p



## I. Specific transcripts markers for non-granulocytes.

Probe set	Accession #	Transcripts	MC.		Ba 1	Ba 2 (small)	Ba 3 (small)	Eo 1	Eo 2	Eo 3 (small)	Eo 4 (small)	Ne 1	Ne 2	Ne 3 (small)	Ne 4 (small)	pl	CD4	CD8	CD14	CD19	Fb
			cord	lung																	
203547_at	U47924	CD4	5.5	4.7	2.2	1.1	1.2	2.0	1.6	0.4	0.9	0.7	1.1	0.7	0.8	3.5	15.0	0.3	17.6	1.2	0.4
205758_at	AW006735	CD8	0.5	1.7	2.6	2.3	3.2	1.3	1.1	2.2	1.7	0.3	0.5	1.8	0.3	4.2	3.0	76.1	0.8	0.6	0.4
206398_s_at	NM_001770.1	CD19	0.7	0.1	0.7	0.4	0.7	0.8	0.5	0.5	0.2	0.6	1.5	1.1	0.7	4.0	0.0	0.1	0.1	19.1	0.4
211644_x_at	L14458.1	IgG V-J region	0.2	0.1	0.1	0.1	0.1	0.2	0.2	0.2	0.3	0.1	0.3	0.2	0.2	3.8	0.1	0.2	0.1	70.9	0.1
201743_at	NM_000591.1	CD14	18.4	2.4	0.3	0.1	0.6	8.8	0.6	1.1	3.2	40.7	49.8	58.7	68.2	2.9	0.4	0.0	97.2	1.1	0.9
203104_at	NM_005211.1	v-fms M-CSF receptor	3.8	0.2	0.6	0.7	0.3	3.0	1.1	1.7	1.5	8.8	8.7	6.3	6.4	5.2	2.8	0.7	42.1	1.4	0.9
209968_s_at	U63041.1	CD56	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.2	0.1	0.1	0.1	0.2	0.1	0.1	0.1	0.1	0.1	0.1	0.0
204627_s_at	M35999.1	CD61 glycoprotein IIIa	1.7	9.4	0.2	0.1	0.3	0.1	0.1	0.1	0.1	0.1	0.4	0.1	0.2	48.3	0.1	0.3	0.1	0.2	0.5
216442_x_at	AK026737.1	fibrinectin	0.3	1.5	0.3	0.3	0.2	0.1	1.0	0.3	0.6	0.1	0.1	0.2	0.1	0.3	0.1	1.0	0.3	0.1	92.6

J. Raw AD levels for the median values used to normalize the raw AD levels, and the housekeeping genes.

Probe set	Accession #	Transcripts	MC. cord blood	MC. lung	Ba 1	Ba 2 (small)	Ba 3 (small)	Eo 1	Eo 2	Eo 3 (small)	Eo 4 (small)	Ne 1	Ne 2	Ne 3 (small)	Ne 4 (small)	pl	CD4	CD8	CD14	CD19	Fb
AFFX-HSAC07X00351_3_at	X00351	beta-actin	18534	19383	14638	20922	19151	22019	18638	21153	18568	19406	22302	16589	17569	18295	18782	20805	20661	17542	20399
AFFX-HSAC07X00351_M_at	X00351	beta-actin	22898	21777	12940	11533	7608	22560	18785	14861	13431	23106	23373	6861	8019	19368	20362	22761	22284	19087	22757
AFFX-HSAC07X00351_5_at	X00351	beta-actin	15642	15838	9516	2927	2066	17186	21061	4861	3771	18772	19768	2165	2193	14887	16381	18218	17583	15063	16795
AFFX-HUMGAPDH/M33197_3_at	M33197	GAPDH	14906	13632	3640	10477	9332	2649	2844	5498	2605	2549	3186	3586	3538	5929	6429	6098	9756	5180	19674
AFFX-HUMGAPDH/M33197_M_at	M33197	GAPDH	15891	16852	3218	7587	6963	2382	2565	3720	1838	2194	2796	2312	2154	6182	5931	5921	11464	4344	17013
AFFX-HUMGAPDH/M33197_5_at	M33197	GAPDH	16298	16701	3479	4559	5110	1827	3121	2127	1168	2492	3476	1636	1355	4655	6826	6260	9905	5636	23350
The median value of 2283 transcripts			121	169.3	85.3	112.2	110.9	93.7	102.1	127.3	114	62.7	73.1	87.4	87.3	82.3	152.5	121.3	107.1	114.1	183.8

Abbreviations used in the table A-I were (small); the results obtained by the small sample protocol (see materials and methods), R; receptor, and ICN; ion channel.